

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:23:17 ; Search time 121.992 Seconds

(without alignments)
779.913 Million cell updates/sec

Title: US-09-250-056b-1

Perfect score: 1300

Sequence: 1 QVQLVSGGGLVQPGSLRL.....YDSLSGWVGSGTKLTVLG 246

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1300	100.0	246	3	AA58235 Internal
2	1292	99.4	291	8	ADN06985 Human EFG
3	1292	99.4	291	8	ADN06984 Human EFG
4	1135.5	87.3	245	8	AD809287 Human C-M
5	1135.5	87.1	251	8	AD812384 Human IGF
6	1125.5	86.6	247	5	ABP45881 Human Bly
7	1125.5	86.6	247	7	ADG96708 Single ch
8	1121.5	86.3	258	8	AD892884 Human Myo
9	1115	85.8	248	8	AD158091 Reg IV-sp
10	1113.5	85.7	247	7	ADG96794 Single ch
11	1113.5	85.7	247	7	ADG96794 Single ch
12	1108	85.2	248	8	AD158045 Reg IV-sp
13	1096.5	84.3	258	8	AD892872 Human Myo
14	1092.5	84.0	247	5	ABP45942 Human Bly
15	1092.5	84.0	247	7	ADG96769 Single ch
16	1092.5	84.0	247	8	AD158094 Reg IV-sp
17	1092	84.0	252	5	ABP45508 Human Bly
18	1092	84.0	252	7	ADG96335 Single ch
19	1086	83.5	277	8	AD025150 Melanoma
20	1084	83.4	238	8	AD809239 Human c-M
21	1082.5	83.3	245	8	AD883864 Chemokine
22	1081	83.2	252	5	ABP45351 Human Bly
23	1081	83.2	252	7	ADG96178 Single ch
24	1080	83.1	258	5	ABP45830 Human Bly
25	1080	83.1	258	7	ADG96657 Single ch

26	1076.5	82.8	243	5	ABP45958 Human Bly
27	1076.5	82.8	243	7	ADG96785 Single ch
28	1075.5	82.7	310	2	AAW83324 Single ch
29	1075.5	82.7	310	5	AB809605 Amino aci
30	1075.5	82.7	310	6	ABG74386 Single ch
31	1075.5	82.7	310	7	ADG98739 Human sIn
32	1075.5	82.7	310	8	AD040448 Human sIn
33	1069	82.2	240	3	AAV15124 Anti-huma
34	1069	82.2	240	3	AAV15125 Anti-muri
35	1069	82.2	252	5	ABP45190 Human Bly
36	1069	82.2	252	7	ADG96017 Single ch
37	1065.5	82.0	262	8	AD892866 Human Myo
38	1062	81.7	250	5	ABP45409 Human Bly
39	1062	81.7	250	7	ADG96236 Single ch
40	1059.5	81.5	253	6	ABJ19830 Human VEG
41	1059.5	81.5	253	8	ADH13872 Human vas
42	1056	81.2	246	6	ABJ19834 Human VEG
43	1056	81.2	246	6	ADH13876 Human vas
44	1053.5	81.0	243	8	AD809284 Human c-M
45	1053	81.0	248	8	AD158058 Reg IV-sp

ALIGNMENTS

RESULT 1	AA58235	standard; protein; 246 aa.
ID	AA58235	standard; protein; 246 aa.
XX	AA58235	
AC	AA58235	
XX	AA58235	
DT	27-MAR-2000	(first entry)
XX	27-MAR-2000	(first entry)
DE	Internalising anti-c-erbB-2 receptor antibody scFv F5.	
XX	Internalising anti-c-erbB-2 receptor antibody scFv F5.	
KW	Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;	
XX	HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.	
OS	Synthetic.	
XX	Synthetic.	
OS	Homo sapiens.	
XX	Homo sapiens.	
PH	Key	Location/Qualifiers
FT	Region	31..35
FT	Region	/note="Heavy chain variable region (VH) complementarity determining region 1 (CDR1)"
FT	Region	50..66
FT	Region	/note="VH-CDR2"
FT	Region	99..108
FT	Region	/note="VH-CDR3"
FT	Region	157..170
FT	Region	/note="VL-CDR2"
FT	Region	186..192
FT	Region	/note="VL-CDR3"
FT	Region	225..235
FT	Region	/note="VL-CDR3"
XX	MO955367-A1.	
XX	MO955367-A1.	
XX	04-NOV-1999.	
XX	04-NOV-1999.	
XX	23-APR-1999.	99WC-US007395.
XX	23-APR-1999.	99WC-US007395.
XX	24-APR-1998.	98US-0082853P.
XX	24-APR-1998.	98US-0082853P.
XX	12-FEB-1999.	99US-00250056.
XX	12-FEB-1999.	99US-00250056.
XX	(REGC) UNIV CALIFORNIA.	
XX	(REGC) UNIV CALIFORNIA.	
XX	Marke UD, Poul MA;	
XX	Marke UD, Poul MA;	
XX	WPI, 2000-072168/06.	
XX	WPI, 2000-072168/06.	
XX	N-PSDB; AA58235.	
XX	N-PSDB; AA58235.	

PT Novel internalizing antibodies used to treat cancer cells.
XX
XX Claim 3; Page 81; 85pp; English.
XX

CC This sequence represents an internalising humanised antibody, scFv F5, which specifically binds to the extracellular domain of the c-erbB-2 receptor, the protein product of the HER/neu oncogene. The scFv F5 antibody binds to the epitope of the c-erbB-2 receptor that is bound by c-erbB-2 antibodies. On binding the c-erbB-2 receptor, the antibody is transported into the cell. The c-erbB-2 receptor is a marker protein which is overexpressed by 30-50% of breast carcinomas and other CC adenocarcinomas, and thus provides a useful cell surface marker for specifically targeting tumour cells. The antibodies of the invention are used as tumour-targeting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin; CC radionuclides; ligands such as growth factors; therapeutic agents such as CC vincristine, vindesine or melphalan; ribozymes; or antisense molecules. CC The antibodies may also be used for in vivo or in vitro detection and/or CC quantitation of the c-erbB-2 receptor and thus diagnosis and/or CC localisation of cancers characterised by expression of c-erbB-2. Although CC antibodies have previously been used to target tumour cells, their CC success has been limited. The utility of prior art antibodies has been CC hampered by the paucity of tumour specific antibodies, antibody CC immunogenicity, low binding affinity, and poor tumour penetration. CC Immunogenicity could be avoided and toxicity reduced if high affinity CC tumour specific human antibodies were available. However, the production CC of human monoclonal antibodies using conventional hybridoma technology CC has proven difficult. Also, most of the antibodies produced react with CC antigens that are also common to non-malignant cells, which makes them CC unsuitable for use as tumour-targeting molecules. The antibodies of the CC invention overcome these difficulties, as they are targeted to a tumour- CC specific antigen, and avoid the problem of immunogenicity as they are CC human in origin
XX
XX

Sequence 246 AA:

Query Match 100.0%; Score 1300; DB 3; Length 246;
Best Local Similarity 100.0%; Pred. No. 3.1e-76;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
QY 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNITY 60
DB 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNITY 60
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKMTSNAFADYWGQGLTVTVSSG 120
DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKMTSNAFADYWGQGLTVTVSSG 120
QY 121 GGGSGGGGSGGGGSGSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 180
DB 121 GGGSGGGGSGGGGSGSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 180
QY 181 KLLIYGNTRPSPGVDPFRFSGFKSGTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 240
DB 181 KLLIYGNTRPSPGVDPFRFSGFKSGTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 240
QY 241 KLTVLG 246
DB 241 KLTVLG 246
```

RESULT 2

ID ADN06985 standard; protein; 291 AA.

ADN06985;

01-JUL-2004 (first entry)

Human EGFR bs-scFv antibody protein, HER3.F4.

Bispecific single chain, bs-scFv; cancer;

KW epidermal growth factor receptor; EGFR; therapy; antibody; human.
XX
XX Homo sapiens.
XX

PN US2004071696-A1.

PD 15-APR-2004.

PF 04-APR-2003; 2003US-00406830.

PR 05-APR-2002; 2002US-0370276P.

PA (REGC) UNIV CALIFORNIA.

PA (FOX-) FOX CHASE CANCER CENT.

PI Adams GP, Horak EM, Weiner LM, Marks JD;

DR WPI; 2004-328525/30.

PT Novel bispecific antibody comprising first and second antibody joined to each other and having binding specificity to different epitopes of PT Epidermal Growth Factor Receptor protein, useful for treating cancer.
XX

PS Claim 14; SEQ ID NO 2; 57pp; English.

XX The present invention provides bispecific single chain (bs-scFv) antibody CC molecules which may be used to treat various forms of cancer associated CC with the overexpression of the epidermal growth factor receptor (EGFR) CC family. The invention is useful for specifically delivering an effector CC molecule to a cell bearing a receptor from EGFR protein family chosen CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the CC treatment of cancer. The present sequence is human EGFR bs-scFv antibody CC protein.
XX
XX

Sequence 291 AA:

Query Match 99.4%; Score 1292; DB 8; Length 291;
Best Local Similarity 99.6%; Pred. No. 1.2e-75;
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```
QY 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNITY 60
DB 23 QVQLVSGGGLVOPGSGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSISRGNITY 82
QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKMTSNAFADYWGQGLTVTVSSG 120
DB 83 ADSVKGRFTISRDNKNTLYLQWNSLRADTAIVYCAKMTSNAFADYWGQGLTVTVSSG 142
QY 121 GGGSGGGGSGGGGSGSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 180
DB 143 GGGSGGGGSGGGGSGSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPGTAP 202
QY 181 KLLIYGNTRPSPGVDPFRFSGFKSGTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 240
DB 203 KLLIYGNTRPSPGVDPFRFSGFKSGTSASLAITGLQADEADYYCCPYDSSLGWFVGGGT 262
QY 241 KLTVLG 246
DB 263 KLTVLG 268
```

RESULT 3

ID ADN06984 standard; protein; 291 AA.

ADN06984;

01-JUL-2004 (first entry)

Human EGFR bs-scFv antibody protein, HER3.F4.

Bispecific single chain, bs-scFv; cancer;

epidermal growth factor receptor; EGFR; therapy; antibody; human.

XX Homo sapiens.
 OS US2004071696-A1.
 XX
 XX 15-APR-2004.
 XX
 XX 04-APR-2003; 2003US-00406830.
 XX
 XX 05-APR-2002; 2002US-0370276P.
 XX
 XX (REGC) UNIV CALIFORNIA.
 XX (FOXC-) FOX CHASE CANCER CENT.
 XX
 XX Adams GP, Horak EM, Weiner LM, Marke JD;
 XX
 XX MPI; 2004-328525/30.
 XX
 XX Novel bispecific antibody comprising first and second antibody joined to
 PT each other and having binding specificity to different epitopes of
 PT Epidermal Growth Factor Receptor protein, useful for treating cancer.
 XX
 XX Claim 14; SEQ ID NO 1, 57bp; English.
 XX
 XX The present invention provides bispecific single chain (bs-scFv) antibody
 CC molecules which may be used to treat various forms of cancer associated
 CC with the overexpression of the epidermal growth factor receptor (EGFR)
 CC family. The invention is useful for specifically delivering an effector
 CC molecule to a cell bearing a receptor from EGFR protein family chosen
 CC from EGFR, HER1/neu, HER3 and HER4. The invention is useful in the
 CC treatment of cancer. The present sequence is human EGFR bs-scFv antibody
 CC protein.
 XX
 XX Sequence 291 AA;

Query Match 99.4%; Score 1292; DB 8; Length 291;
 Best Local Similarity 99.6%; Pred. No. 1.2e-75;
 Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQLVSSGGGLVOPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGRGNTYY 60
 DB 23 QVQLVSSGGGLVOPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGRGNTYY 82
 QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTVAVYYCAKMTSNAPFDYWGQGLTVTVSSG 120
 DB 83 ADSVKGRFTISRDNKNTLYLQNSLRADTVAVYYCAKMTSNAPFDYWGQGLTVTVSSG 142
 QY 121 GGGSGGGSGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQQLPETA 180
 DB 143 GGGSGGGSGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQQLPETA 202
 QY 181 KLLIYNTNRPSPGVPRFSGFGKSTASALITGLQADEADYYCCQYDSSLSWVGGGT 240
 DB 203 KLLIYNTNRPSPGVPRFSGFGKSTASALITGLQADEADYYCCQYDSSLSWVGGGT 262
 QY 241 KLTVLG 246
 DB 263 KLTVLG 268

RESULT 4
 ADS09297
 ID ADS09297 standard; protein; 245 AA.
 XX
 XX ADS09297;
 XX
 XX 18-NOV-2004 (first entry)
 XX
 XX Human c-Met protein tyrosine kinase antibody, PGTA-4-A12.
 DE c-Met; tyrosine kinase antibody; antigen binding; cytosolic;
 XX ophthalmological; antiinflammatory; analgesic; vasodilator; antiproliferatic;
 KW osteopathic; cancer; tumour; ophthalmic disease; glaucoma; retinitis;

KM retinopathy; uveitis; ocular photophobia; macular degeneration; pain;
 KM acute injury; eye; hyperproliferative disorder; restenosis; angioplasty;
 KM psoriasis; HGF; osteoporosis; cancer.
 XX

OS Homo sapiens.
 XX
 XX MO2004072117-A2.
 XX
 XX 26-AUG-2004.
 XX
 XX 11-FEB-2004; 2004MO-IB000503.
 XX
 XX 13-FEB-2003; 2003US-0447073P.
 XX
 XX (PHAA) PHARMACIA CORP.
 XX
 XX Norton PA, Arbuckle JA, Evans ML, Joy WD, Kahn LE, Shieh JJ;
 XX
 XX MPI; 2004-616044/59.
 XX
 XX N-PDB; ADS09357.
 XX

PT Novel c-Met protein tyrosine kinase antibody or its antigen-binding
 PT portion specifically binding to c-Met, useful for manufacture of
 PT medicament for treating cancer or tumor and for treatment of ophthalmic
 PT diseases such as glaucoma.
 XX
 XX Claim 1; SEQ ID NO 59; 303bp; English.
 XX
 XX The invention relates to a novel c-Met protein tyrosine kinase antibody
 CC or its antigen binding portion that specifically binds to c-Met. The c-
 CC Met antibody comprises any one of 1-60 fully defined sequence of 238,
 CC 244, 240, 250, 251, 242, 245, 247, 246, 253, 249, 243, 241, etc., amino
 CC acids as given in the specification, or its fragment. The invention
 CC further comprises: a pharmaceutical composition comprising the c-Met
 CC protein tyrosine kinase antibody and a carrier; an isolated cell that
 CC produces the c-Met protein tyrosine kinase antibody; and an isolated
 CC nucleic acid molecule that comprises a nucleic acid sequence that encodes
 CC a heavy chain or its antigen-binding portion or light chain or its
 CC antigen-binding portion of the c-Met protein tyrosine kinase antibody.
 CC
 CC The c-Met protein tyrosine kinase antibody has cytostatic,
 CC ophthalmological, antiinflammatory, analgesic, vasodilator, antiproliferatic,
 CC and osteopathic activities. The c-Met protein tyrosine kinase antibody is
 CC useful for the manufacture of medicament for the treatment of cancer or
 CC tumour. The c-Met protein tyrosine kinase antibody is useful for
 CC diagnosing the presence or ligation of c-Met expressing tissue. The c-Met
 CC protein tyrosine kinase antibody is useful for detecting c-Met in a
 CC biological sample in vitro or in vivo. The c-Met protein tyrosine kinase
 CC antibody is also useful in the treatment or prevention of ophthalmic
 CC diseases such as glaucoma, retinitis, retinopathies (e.g., diabetic
 CC retinopathy), uveitis, ocular photophobia, macular degeneration and pain
 CC associated with acute injury to the eye. The pharmaceutical composition
 CC is useful for the treatment of hyperproliferative disorders such as
 CC restenosis after angioplasty, and psoriasis, and for the treatment of
 CC animals that lack sufficient HGF, e.g. osteoporosis and cancer. This
 CC sequence represents the protein of a phage display generated human c-Met
 CC antibody of the invention.
 XX
 XX Sequence 245 AA;

Query Match 87.3%; Score 1135.5; DB 8; Length 245;
 Best Local Similarity 88.7%; Pred. No. 1.3e-65;
 Matches 219; Conservative 10; Mismatches 15; Indels 3; Gaps 2;

QY 1 QVQLVSSGGGLVOPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGRGNTYY 60
 DB 1 EVQLLESGGGLVOPGSLRLSCAASGFTPRSYAMSVWRQAPGKLEWVSAISGGGNTYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADTVAVYYCAKMTSNAPFDYWGQGLTVTVSSG 120
 DB 61 ADSVKGRFTISRDNKNTLYLQNSLRADTVAVYYCAKMTSNAPFDYWGQGLTVTVSSG 118
 QY 121 GGGSGGGSGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQQLPETA 179

	Matches	218;	Conservative	13;	Mismatches	15;	Indels	5;	Gaps	2
QY	1	QV	LVESGGGLV	QGGSLRLSCAASGFFFRSYAMSWNRQAQGGKGLIEWSAISGRDNTMY	60					
Db	1	EV	LLLESGGGIV	QGGSLRLSCAASGFFFRSYAMSWNRQAQGGKGLIEWSAISGGSGSTYY	60					
QY	61	AD	VKGRFTISR	DSKNTLYIQNNMSLRADPAVYYCAKWT---SNAFAFDYWGQTLVT	116					
Db	61	AD	VKGRFTISR	DSKNTLYIQNNMSLRADPAVYYCAASPPPMADWYTFDYWGQTLVT	120					
QY	117	VSS	GGGGSGGGSGGGGS-QEVLTPPSVSA	PGQRTVITSGTSSSNIGAGYGVHWYQQL	175					
Db	121	VSS	GGGGSGGGSGGGSGAQLVLPQPSVSGA	PGQRTVITSGTSSSNIGAGYGVHWYQQL	180					
QY	176	PGT	APKLLIYNTN	RPSGVDPFRFGSGKGTSAISLAITGLQADEADYTCQFDSSLSGMY	235					
Db	181	PGT	APKLLIYNTN	RPSGVDPFRFGSGRGTSAISLAITGLQADEADYTCQSDSNISGSV	240					
QY	236	FGG	GTKLTVLG	246						
Db	241	FGG	GTKTVLVG	251						
RESULT 6										
ABP45881										
ID	ABP45881	standard; protein; 247 AA.								
XX	ABP45881;									
AC	19-AUG-2002	(first entry)								
DT	19-AUG-2002	(first entry)								
XX	Human Blys binding scFv SEQ ID 1892.									
DE	Human Blys binding scFv SEQ ID 1892.									
XX	Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;									
KW	tumour necrosis factor; B cell proliferation; B cell differentiation;									
KW	immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;									
KW	antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;									
KW	systemic lupus erythematosus; rheumatoid arthritis; CYID; AIDS;									
KW	common variable immunodeficiency; acquired immunodeficiency syndrome.									
XX	Homo sapiens.									
OS	Homo sapiens.									
XX	WO200202641-A1.									
PN	10-JAN-2002.									
PD	10-JAN-2002.									
XX	15-JUN-2001; 2001WO-US019110.									
PF	15-JUN-2001; 2000US-0212210P.									
XX	16-JUN-2000; 2000US-0212210P.									
PR	17-OCT-2000; 2000US-0240818P.									
PR	16-MAR-2001; 2001US-0276248P.									
PR	21-MAR-2001; 2001US-0277379P.									
PR	25-MAY-2001; 2001US-0293499P.									
XX	(HUMA-) HUMAN GENOME SCI INC.									
PA	(CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.									
XX	Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;									

CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX Sequence 247 AA;

SO Query Match

Best Local Similarity 86.4%; Score 1125.5; DB 5; Length 247;
 Matches 216; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAAGFTRSYMSVWRQAPGKLEWVAISGRGNTYY 60
 DB 1 QVTLKESGDLVPGGSLRLSCAAGLTFTMSYMTWRQAPGKLEWVAISGSGDNTYY 60
 QY 61 ADSVKGRTISRDNSKNTLYLQWNSLRADTAAYYCAKMTSNAPFDYWGQTLVTVSSG 120
 DB 61 GDSVGRFTISRDNKNTLYFLQWNSLRADTAAYYCAKHTGYAEENMGRGLTVTVSSG 120
 QY 121 GGGSGGGSGGGGGS-OSVLTQPPSVGAPGQRTVTSCTGSSSNIGAGYGVHWYQQLPGTA 179
 DB 121 GGGSGGGSGGGGGSASVLTQPPSVGAPGQRTVTSCTGSSSNIGAGYGVHWYQQLPGTA 180
 QY 180 PKLLIYGNTRPESGVDPRFSGKTSASLAIITGLQAEDEADYYCQPYDSSLGFWFGG 239
 DB 181 PRLLISNTNRPESGVDPRFSGSKTSASLAIITGLQAEDEADYYCQSYDSSLGFWFGTG 240
 QY 240 TKLTVLG 246
 DB 241 TKYTVLG 247

RESULT 7
 ADG96708

ID ADG96708 standard; protein; 247 AA.

AC ADG96708;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds BlyS SeqID 1892.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antiinflammatory; antiallergic; antiallergic; cytostatic.

XX Unidentified.

OS Unidentified.

PN MO2003055979-AA2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002MO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX MPI; 2003-505530/47.
 DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (BlyS), useful for detecting and treating diseases or disorders e.g.

PT rheumatoid arthritis, asthma and leukemia.
 XX Example 1; SEQ ID NO 1892; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (BlyS). The BlyS gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scfv) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey BlyS. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of BlyS or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiarthritic, neuroprotective,
 CC antiinflammatory, antiallergic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds BlyS of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIP0 at fcp.wipo.int/pub/published pct_sequences.

XX Sequence 247 AA;

SO Query Match

Best Local Similarity 86.4%; Score 1125.5; DB 7; Length 247;
 Matches 216; Conservative 12; Mismatches 18; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAAGFTRSYMSVWRQAPGKLEWVAISGRGNTYY 60
 DB 1 QVTLKESGDLVPGGSLRLSCAAGLTFTMSYMTWRQAPGKLEWVAISGSGDNTYY 60
 QY 61 ADSVKGRTISRDNSKNTLYLQWNSLRADTAAYYCAKMTSNAPFDYWGQTLVTVSSG 120
 DB 61 GDSVGRFTISRDNKNTLYFLQWNSLRADTAAYYCAKHTGYAEENMGRGLTVTVSSG 120
 QY 121 GGGSGGGSGGGGGS-OSVLTQPPSVGAPGQRTVTSCTGSSSNIGAGYGVHWYQQLPGTA 179
 DB 121 GGGSGGGSGGGGGSASVLTQPPSVGAPGQRTVTSCTGSSSNIGAGYGVHWYQQLPGTA 180
 QY 180 PKLLIYGNTRPESGVDPRFSGKTSASLAIITGLQAEDEADYYCQPYDSSLGFWFGG 239
 DB 181 PRLLISNTNRPESGVDPRFSGSKTSASLAIITGLQAEDEADYYCQSYDSSLGFWFGTG 240
 QY 240 TKLTVLG 246
 DB 241 TKYTVLG 247

RESULT 8
 ADS92884

ID ADS92884 standard; protein; 258 AA.

AC ADS92884;

DT 02-DEC-2004 (first entry)

DE Human Myo28 antibody single chain Fv fragment (scfv) germlined protein.

XX Human; Myo28; single chain Fv fragment; scfv;
 KW growth and differentiation factor-8; GDF-8;
 KW bone morphogenetic protein-11; BMP-11; muscle strength; muscle mass;
 KW ActRIIB; muscle repair; glucose tolerance; neuromuscular disorder;
 KW bone degenerative disorder; muscular dystrophy;
 KW Duchenne muscular dystrophy; organ atrophy;
 KW carpal tunnel syndrome; congestive obstructive pulmonary disease;
 KW cachexia; muscle wasting syndrome; amyotrophic lateral sclerosis;
 KW obesity; adipose tissue disorder; syndrome X; impaired glucose tolerance;

XX	trauma-induced insulin resistance; type 2 diabetes; myocardial muscle;
KW	diaphragm muscle; antibody; germlined protein.
XX	
OS	Homo sapiens.
XX	
PN	MO2004037861-A2.
XX	
PD	06-MAY-2004.
XX	
PE	22-OCT-2003; 2003MO-IB004748.
XX	
XX	22-OCT-2002; 2002US-0419964P.
PR	
PA	(AMHP) WYETH-
XX	(CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
PI	Veldman GM, Davies MV, Song K, Wolfman NM, Grove-Bridges K;
DR	Field A, Russell C, Valge-Archer V;
XX	WP1; 2004-365497/34.
DR	N-PSDB; ADS92883.
XX	
PT	New antibody that binds GDF-8 or BMP-11, useful in preparing a
PT	composition for repairing damaged muscle, increasing muscle mass or
XX	strength or increasing glucose tolerance in a mammal.
PS	
XX	Claim 1; SEQ ID NO 20; 117pp; English.
CC	The invention relates to an antibody that is capable of specifically
CC	binding growth and differentiation factor-8 (GDF-8) or bone morphogenetic
CC	protein-11 (BMP-11). The invention also relates to a pharmaceutical
CC	composition comprising the antibody, an isolated nucleic acid encoding
CC	the antibody, a method of making an antibody that specifically reacts
CC	with GDF-8, a method of identifying inhibitors of GDF-8 and a method of
CC	increasing muscle strength or mass comprising administering the antibody.
CC	The antibody is an scFv fragment expressed by Escherichia coli, capable
CC	of inhibiting binding of GDF-8 to Acvr1b. The amino acid sequence of the
CC	antibody is modified to reduce or alter effector function. The antibody
CC	is useful in preparing a composition for repairing damaged muscle,
CC	increasing muscle mass or strength or increasing glucose tolerance in a
CC	mammal, or for treating or preventing neuromuscular disorders, bone
CC	degenerative disorders, muscular dystrophy, Duchenne muscular dystrophy,
CC	obstructive pulmonary disease, cachexia, carpal tunnel syndrome, congestive
CC	amyotrophic lateral sclerosis, obesity, adipose tissue disorder, syndrome
CC	X, impaired glucose tolerance, trauma-induced insulin resistance, type 2
CC	diabetes and damaged myocardial or diaphragm muscle. This sequence
CC	represents the human Myo28 antibody single chain Fv fragment (scFv)
CC	germlined protein of the invention.
XX	
XX	Sequence 258 AA;
QY	
QY	Query Match 86.3%; Score 1121.5; DB 8; Length 258;
QY	Best Local Similarity 86.3%; Pred. No. 1.1e-64;
QY	Matches 215; Conservative 13; Mismatches 18; Indels 3; Gaps 2
DB	
QY	1 OVVLVESGGGLVDPGSGSLRLCAAGFTRSYAMGVNRAPKGLGEWVAISGRGNTYY 60
DB	1 EQQLLESGGGLVDPGSGSLRLCAAGFTRSRVYVMVRAPGKGLGEWVAISVGGSTAY 60
QY	61 ADVYKGRFTISHDNSKNTLYLQMSLRADETAVYYCAK--MTSNAPAFDPYWGSGTLVTVS 118
DB	61 ADVYKGRFTISHDNSKNTLYLQMSLRADETAVYYCAKQWMEGSGYTFDYWKRGTLVTVS 120
QY	119 SGGGSGGGGGSGGGGS-QSVLTQPPSVSGAPGQRTVISTGSSSNIGAGYGVHWYQQLPG 177
DB	121 SGGGSGGGGGSGGGGSQAQSVLTQPPSVSGAPQRTVISTGSSSNIGAGYGVHWYQQLPG 180
QY	178 TAPKLLIYGNTRPSPGVPRFGFSGTASALATGLQMEDADADYYCCQYDSSLGQWPG 237
DB	181 TAPKLLIYGNTRPSPGVPRFGFSGTASALATGLQMEDADADYYCHSYDGSVSGMIFG 240
QY	238 GGTKLTIVG 246

Db	241	GGTKLTVLG	249
XX	ADIS8091	standard; protein; 248 AA.	
XX	ADIS8091;		
XX	22-APR-2004	(first entry)	
XX	Reg IV-specific single chain antibody fragment (scFv) #50.		
XX	antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;		
XX	inflammatory bowel disorder; ulcerative colitis; Crohn's disease;		
XX	diabetes; non-insulin dependent diabetes; insulin dependent diabetes;		
XX	cancer; human.		
XX	Homo sapiens.		
XX	MO2004003144-A2.		
XX	08-JAN-2004.		
XX	26-JUN-2003; 2003WO-US019908.		
XX	01-JUL-2002; 2002US-0392382P.		
XX	(HUMA-) HUMAN GENOME SCI INC.		
XX	Rosen CA;		
XX	WPI; 2004-071976/07.		
XX	DR N-PSDB; ADI58157.		
XX	Novel antibody, useful for treating, preventing or ameliorating		
XX	inflammatory bowel disorder, cancer of the gastrointestinal tract or		
XX	diabetes (non-insulin dependent diabetes or insulin dependent diabetes).		
XX	Claim 2; SEQ ID NO 51; 324dp; English.		
XX	The invention comprises an antibody that specifically binds a		
XX	regeneration IV (Reg IV) protein. The invention specifically comprises		
XX	the amino acid and coding sequences of single chain antibody fragments		
XX	(scFv's) that bind Reg IV protein. The antibody of the invention is		
XX	useful for treating, preventing and ameliorating: inflammatory bowel		
XX	disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.		
XX	non-insulin dependent diabetes or insulin dependent diabetes), and cancer		
XX	of the gastrointestinal tract. The antibody of the invention is also		
XX	useful for detecting the expression of a Reg IV protein. The present		
XX	amino acid sequence represents an scFv of the invention.		
XX	Sequence 248 AA;		
XX	Query Match 85.8%; Score 115; DB 8; Length 248;		
XX	Best Local Similarity 88.7%; Pred. No. 2,7e-64;		
XX	Matches 220; Conservative 7; Mismatches 19; Indels 2; Gaps 2;		
QY	1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSATISGRDNTYY 60		
DB	1 EVQLLESGGGLVQPGGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGSTYY 60		
QY	61 ADSVKGFTTISRDKSKNTLYIQMNSLAEPDAVYYCARVYSGLLDAPIDWQGTIVVSS 119		
DB	61 ADSVKGFTTISRDKSKNTLYIQMNSLAEPDAVYYCARVYSGLLDAPIDWQGTIVVSS 120		
QY	120 GGGSGGGSGGGSGGS-OSVLTQPPSVGAPGQRVTIISCTGSSNIGAGYVHWYQOLPGT 178		
DB	121 GGGSGGGSGGGSGGSASVLTQPPSVGAPGQRVTIISCTGSSNIGAGNDVHWYQVPGR 180		
QY	179 APKLLIYGNTNRPGVDPDRSGFSGTSSALITGLQADIEDADYYCOFYDSSLSGWTFFG 238		

DB 181 APELLIYGTTPSPGVDRFSGSGKSTASLAITGLQAEADYFCOSDDSLSGSVFG 240

QY 239 GTRLTFLG 246

DB 241 GTRLTFLG 248

RESULT 10

ABP45967

ID ABP45967 standard; protein; 247 AA.

AC ABP45967;

DT 19-AUG-2002 (first entry)

XX Human Blys binding scfv seq ID 1978.

DE Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

OS MO200202641-A1.

PN 10-JAN-2002.

PD 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

PR 25-MAY-2001; 2001US-0293499P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2760-2761; 3148pp; English.

XX This invention describes novel antibodies that immunospecifically bind to B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of Blys. The antibodies bind to Blys and so may be used to detect and quantitate the presence of Blys in biological samples and may be used in this way to diagnose disease associated with aberrant expression of Blys. They may also be administered to treat diseases associated with aberrant Blys expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the invention

XX Sequence 247 AA;

QY Query Match 85.7%; Score 1113.5; DB 5; Length 247;

XX Best Local Similarity 85.8%; Pred. No. 3,4e-54;

XX Matches 212; Conservative 14; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSVRQAPGKLEWVAISRGCDNTYY 60

DB 1 EVQLVETGGGLVQPGGSLRLSCAASGFTSSYAMTVRQAPGKLEWVAISNGSNTTH 60

QY 61 ADSVKGRFTTISHDNRKNTLYLQMNLSIRADTAIVYICAKRTSNAPFDYNGGTLVTSSG 120

DB 61 ADFVKGRTFTASDNRKSLIYLQMNLSLTADDSAVYICAKYNGFYFEYNGGTLVTSSG 120

QY 121 GGGSGGGSGGGGGS-QSVLTQPPSVGARGQVTTISCTSSSSNIGYGVHWYQQLPRTA 179

DB 121 GGGSGGGSGGGGSAQSVLTQPPSVGARGQVTTISCTSSSSNIGYGVHWYQQLPRTA 180

QY 180 PKLLIYGNTRRPSGVDRFSGSGKSTASLAITGLQAEADYFCOYFSSSLSGWFGG 239

DB 181 PKLLIFGNRRPSGVDRFSGSGKSTASLAITGLQPDDEADYFCOYFSSSLSGWFGG 240

QY 240 TKLTVLG 246

DB 241 TKLTVLG 247

RESULT 11

ADG96794

ID ADG96794 standard; protein; 247 AA.

AC ADG96794;

DT 11-MAR-2004 (first entry)

XX Single chain antibody that immunospecifically binds Blys seqid 1978.

DE Blys; B lymphocyte stimulator; Blys; tumour necrosis factor; B cell proliferation; differentiation; scfv; myasthenia gravis; multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia; carcinoma; lymphoma; antirheumatic; antirheumatic; neuroprotective; antiinflammatory; antiaesthetic; antiasthergic; cytostatic.

XX Unidentified.

OS WO2003055979-A2.

PN 10-JUL-2003.

PD 14-NOV-2002; 2002WO-US036496.

PF 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

XX (HUMA-) HUMAN GENOME SCI INC.

PA Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

XX WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator (Blys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1978; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (Blys). The Blys gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scfvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey Blys. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of Blys or its receptor. As such, these compositions are useful for identifying immune disorders

PA (AMRP) WYETH.
PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX Veldman GM, Davies MV, Song K, Wolman NM, Grove-Bridges K;
PI Field A, Russell C, Valge-Archer V;
XX WPI; 2004-365497/34.
DR N-PSDB; ADS92871.
XX
XX New antibody that binds GDF-8 or BMP-11, useful in preparing a
PT composition for repairing damaged muscle, increasing muscle mass or
PT strength or increasing glucose tolerance in a mammal.
XX
XX Claim 1; SEQ ID NO 8; 117pp; English.
XX
XX The invention relates to an antibody that is capable of specifically
CC binding growth and differentiation factor-8 (GDF-8) or bone morphogenetic
CC protein-11 (BMP-11). The invention also relates to a pharmaceutical
CC composition comprising the antibody, an isolated nucleic acid encoding
CC the antibody, a method of making an antibody that specifically reacts
CC with GDF-8, a method of identifying inhibitors of GDF-8 and a method of
CC increasing muscle strength or mass comprising administering the antibody.
CC The antibody is an scFv fragment expressed by *Escherichia coli*, capable
CC of inhibiting binding of GDF-8 to ActRIIb. The amino acid sequence of the
CC antibody is modified to reduce or alter effector function. The antibody
CC is useful in preparing a composition for repairing damaged muscle,
CC increasing muscle mass or strength or increasing glucose tolerance in a
CC mammal, or for treating or preventing neuromuscular disorders, bone
CC degenerative disorders, muscular dystrophy, Duchenne muscular dystrophy,
CC muscular atrophy, organ atrophy, carpal tunnel syndrome, congestive
CC obstructive pulmonary disease, cachexia, muscle wasting syndrome,
CC amyotrophic lateral sclerosis, obesity, adipose tissue disorder, syndrome
CC X, impaired glucose tolerance, trauma-induced insulin resistance, type 2
CC diabetes and damaged myocardial or diaphragm muscle. This sequence
CC represents the human Myo28 antibody single chain Fv fragment (scFv) of
CC the invention.
XX
XX Sequence 258 AA;
SQ

Query Match 84.3%; Score 1096.5; DB 8; Length 258;
Best Local Similarity 84.7%; Pred. No. 4,4e-63;
Matches 211; Conservative 12; Mismatches 23; Indels 3; Gaps 2;

QY 1 QVALVESGGGLVQPGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVAISGRGNTYY 60
DB 1 QVTLESQGGGLVQPGSLRLSCAASGFTSRVYINVRQAPGKLEWVAISVGGSTAY 60
QY 61 ADSVKGRTFTISRDNSTNTLYLQNSLRADTAAYCTKQWMERGSYYPYMGRTLVTVS 118
DB 61 ADSVKGRTFTISRDNSTNTLYLQNSLRADTAAYCTKQWMERGSYYPYMGRTLVTVS 120
QY 119 SGGGSGGGGSGGGGSG-OSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQOLPG 177
DB 121 SGGGSGGGGSGGGGSAQSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQOLPG 180
QY 178 TAPKLLIYGNTRPSGVPDRFSGFGKSGTASLAITGLQAEDEADYYCQFYDSSLGWFVG 237
DB 181 TAPKLLIYGNTRPSGVPDRFSGFGKSGTASLAITGLQAEDEADYYCQFYDSSLGWFVG 240
QY 238 GGTKLTVLG 246
DB 241 GGTKLTVLG 249

RESULT 14
ABP45942
ID ABP45942 standard; protein; 247 AA.
XX
XX ABP45942;
AC
XX
XX
DT 19-AUG-2002 (first entry)
XX
DE Human Blys binding scFv SEQ ID 1953.

XX
XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
KM tumour necrosis factor; B cell proliferation; B cell differentiation;
KM immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
KM antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.
OS
XX Homo sapiens.
XX
XX MO200202641-A1.
XX
XX 10-JAN-2002.
XX
XX 15-JUN-2001; 2001WO-US019110.
XX
XX 16-JUN-2000; 2000US-0212210P.
XX
XX 17-OCT-2000; 2000US-0240816P.
XX
XX 16-MAR-2001; 2001US-0276248P.
XX
XX 21-MAR-2001; 2001US-0277379P.
XX
XX 25-MAY-2001; 2001US-0293499P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
XX WPI; 2002-114799/15.
XX
XX Antibodies against B lymphocyte stimulating polypeptides, useful for the
PT diagnosis and treatment of cancers and immune disorders.
XX
XX
XX Claim 1; Page 2731-2732; 3148pp; English.
XX
XX This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antirheumatic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention.
XX
XX Sequence 247 AA;
SQ

Query Match 84.0%; Score 1092.5; DB 5; Length 247;
Best Local Similarity 85.8%; Pred. No. 7,6e-63;
Matches 212; Conservative 10; Mismatches 24; Indels 1; Gaps 1;

QY 1 QVALVESGGGLVQPGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVAISGRGNTYY 60
DB 1 EVOLVESGGGLVQPGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVAISVGGATYY 60
QY 61 ADSVKGRTFTISRDNSTNTLYLQNSLRADTAAYCAKMTSNAPFDYGGGLTVVSSG 120
DB 61 ADSVKGRTFTISRDNSTNTLYLQNSLRADTAAYCAKMTSNAPFDYGGGLTVVSSG 120
QY 121 GGGSGGGGSGGGGSG-OSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQOLPGTA 179
DB 121 GGGSGGGGSGGGGSAQSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYGVHWYQOLPGTA 180
QY 180 PKLLIYGNTRPSGVPDRFSGFGKSGTASLAITGLQAEDEADYYCQFYDSSLGWFVG 239
DB 181 PKVLIYGNTRPSGVPDRFSGFGKSGTASLAITGLQAEDEADYYCQFYDSSLGWFVG 240

OY 240 TKLVVLG 246
 DB 241 TKLVVLG 247

RESULT 15

ID ADG96769 standard; protein; 247 AA.

AC ADG96769;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys segid 1953.

KM antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
 KW carcinoma; lymphoma; antirheumatic; antiallergic; neuroprotective;
 KW antinflammatory; antiaesthetic; antiallergic; cytostatic.

OS Unidentified.

PN WO2003055979-A2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-0331469P.

PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

DR WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1953; 394pp; English.

CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scfvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiallergic, neuroprotective,
 CC antinflammatory, antiaesthetic, antiallergic and cytostatic. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.

XX Sequence 247 AA;

Query Match 84.0%; Score 1092.5; DB 7; Length 247;
 Best Local Similarity 85.8%; Pred. No. 7.6e-63;
 Matches 212; Conservative 10; Mismatches 24; Indels 1; Gaps 1;

OY 1 QVQLVSGGGLVQPGSRLRLSCAAGFTFRSYAMSWVRQAPGKLEWVSALISGRDNTYY 60
 DB 1 EVQLVESGGGLVQPGMSLRSLSCAAGFTFRSYSAMTWVRQAPGKLEWVSALISGGATYY 60
 OY 61 ADSVKGRTFISRDNSKNTLYIQMNSLRADTAIVYYCAKRTSNAPAFDVGCGTLVTVSSG 120
 DB 61 ADSVKGRTFISRDNSKNTLYIQMNSLRADTAIVYYCAKRTSNAPAFDVGCGTLVTVSSG 120
 OY 121 GGGSGGGSGGGGS-QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYGVHWYQQLPGTA 179
 DB 121 GGGSGGGSGGGGSASQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYGVHWYQQLPGTA 180
 OY 180 PKLLIYGNTNRPSGVPPDRFGSKSGTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGG 239
 DB 181 PKVLIYGNRNRPSSGVPPDRFGSKSGTSASLAITGLQAEDEADYYCQSYDRSLRAFAVFGTG 240
 OY 240 TKLVVLG 246
 DB 241 TKLVVLG 247

Search completed: April 19, 2005, 16:39:11
 Job time : 123.992 secs

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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:32:47 ; Search time 30.2459 seconds
(without alignments)
607.146 Million cell updates/sec

Title: US-09-250-056B-1

Perfect score: 1300
Sequence: 1 QVQLVSGGGLVQPGGSLRL.....YDSISLGWFGGGTTLTVLG 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-Processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 2: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 3: /cgn2_6/prodata/1/iaa/5A_COMB.pep:*
- 4: /cgn2_6/prodata/1/iaa/5B_COMB.pep:*
- 5: /cgn2_6/prodata/1/iaa/PCTUS_COMB.pep:*
- 6: /cgn2_6/prodata/1/iaa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1075.5	82.7	310	3	US-09-079-029-11 Sequence 11, Appl
2	1017.5	78.3	334	4	US-09-046-028-53 Sequence 53, Appl
3	1017.5	78.3	339	4	US-09-046-028-55 Sequence 55, Appl
4	1017.5	78.3	348	4	US-09-046-028-51 Sequence 51, Appl
5	892.5	68.7	312	3	US-09-079-029-10 Sequence 10, Appl
6	887	68.0	358	2	US-09-079-029-9 Sequence 9, Appl
7	883.5	68.0	358	2	US-08-665-202-5 Sequence 5, Appl
8	883.5	68.0	258	4	US-09-315-574-5 Sequence 5, Appl
9	855	65.8	240	4	US-09-192-854-2 Sequence 2, Appl
10	852.5	65.6	280	3	US-09-260-527-1 Sequence 1, Appl
11	841.5	64.7	281	3	US-09-025-769B-178 Sequence 178, App
12	841.5	64.7	281	4	US-09-490-070A-178 Sequence 178, App
13	841.5	64.7	281	4	US-09-490-153-178 Sequence 178, App
14	841.5	64.7	281	4	US-09-490-324-178 Sequence 178, App
15	827	63.6	268	4	US-09-976-118-1 Sequence 1, Appl
16	819.5	63.0	245	4	US-08-918-148-75 Sequence 75, Appl
17	819.5	63.0	245	4	US-09-138-091A-73 Sequence 73, Appl
18	794.5	61.1	245	4	US-08-918-148-78 Sequence 78, Appl
19	793.5	61.0	245	4	US-09-138-091A-76 Sequence 76, Appl
20	792.5	61.0	245	3	US-08-918-148-76 Sequence 76, Appl
21	792.5	61.0	245	4	US-09-138-091A-74 Sequence 74, Appl
22	791.5	60.9	249	3	US-08-918-148-74 Sequence 74, Appl
23	791.5	60.9	249	4	US-09-138-091A-72 Sequence 72, Appl
24	781	60.1	244	3	US-08-918-148-77 Sequence 77, Appl
25	781	60.1	244	4	US-09-138-091A-75 Sequence 75, Appl
26	768	59.1	236	4	US-08-190-199A-65 Sequence 65, Appl
27	768	59.1	244	3	US-08-918-148-79 Sequence 79, Appl

28	768	59.1	244	4	US-09-138-091A-77 Sequence 77, Appl
29	765	58.8	301	2	US-08-661-052-14 Sequence 14, Appl
30	765	58.8	301	3	US-09-188-082-14 Sequence 14, Appl
31	765	58.8	301	3	US-09-364-088-14 Sequence 14, Appl
32	765	58.8	301	3	US-09-102-716-14 Sequence 14, Appl
33	765	58.8	553	2	US-08-661-052-16 Sequence 16, Appl
34	765	58.8	553	3	US-09-188-082-16 Sequence 16, Appl
35	765	58.8	553	3	US-09-364-088-16 Sequence 16, Appl
36	765	58.8	553	3	US-09-102-716-16 Sequence 16, Appl
37	756	58.2	240	2	US-08-956-047-25 Sequence 25, Appl
38	747	57.5	255	3	US-09-553-498-8 Sequence 8, Appl
39	747	57.5	255	4	US-09-618-869-8 Sequence 8, Appl
40	740.5	57.0	240	1	US-08-488-113B-148 Sequence 148, App
41	740.5	57.0	240	1	US-08-477-484B-148 Sequence 148, App
42	740.5	57.0	240	2	US-08-646-360-148 Sequence 148, App
43	740.5	57.0	240	3	US-08-839-765-148 Sequence 148, App
44	740.5	57.0	240	3	US-09-136-389-148 Sequence 148, App
45	740.5	57.0	240	3	US-09-610-838-148 Sequence 148, App

ALIGNMENTS

RESULT 1
US-09-079-029-11
; Sequence 11, Application US/09079029
; Patent No. 6342369
; GENERAL INFORMATION:
; APPLICANT: Adams, Camilla W.
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Chuntarapai, Anan
; APPLICANT: Kim, Kyung J.
; TITLE OF INVENTION: Apo-2 Receptor
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,029
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Matschang, Diane L.
; REGISTRATION NUMBER: 35,600
; REFERENCE/DOCKET NUMBER: P1101R2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/952-5416
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 310 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-09-079-029-11
Query Match 82.7%; Score 1075.5; DB 3; Length 310;
Best Local Similarity 84.6%; Pred. No. 3.7e-75;
Matches 208; Conservative 11; Mismatches 26; Indels 1; Gaps 1;
QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSRYSAMVRQAPKGLWEVSAISGRGDNITY 60
DB 40 QVQLVSGGGLVQPGGSLRLSCAASGFTSRYSAMVRQAPKGLWEVSAISGRGDNITY 99
QY 61 ADVKGRFTISRDNKNTLYLQMNLSLRADTVVYCAKNTSNAPFAFDYWGQGLTVTVSSG 120

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Db 100 ADSVKGRFTISRDNSKNTLYLQNNLSRAEDTAVYYCAR-DRGYVMDVWGKGTITLVSSG 158
QY 121 GGGSGGGGGGGSSGVLTQPPSVSGAPGQRTVISTCGSSSNIGAGYVHWYQQLGTP 180
Db 159 GGGSGGGGGGGSSGVLTQPPSVSGAPGQRTVISTCGSSSNIGAGYVHWYQQLGTP 218
QY 181 KLIIYGNTRPSGVPRFSGFGKSGTSASLAITGLQADEADYVCOFYDSSLGWFVGGGT 240
Db 219 KLIIYDSDNRPSGVPRFSGFGKSGTSASLAITGLQADEADYVCOFYDSSLGWFVGGGT 278
QY 241 KLTVLG 246
Db 279 KTVLIG 284

RESULT 2
US-09-646-028-53
; Sequence 53, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsayn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 334
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-53

Query Match 78.3%; Score 1017.5; DB 4; Length 334;
Best Local Similarity 79.8%; Pred. No. 1.2e-70;
Matches 198; Conservative 13; Mismatches 34; Indels 3; Gaps 2;

QY 1 QVOLVESGGGLVOPGGSLRLSCAASGFTPRSYAMSWVROAPGKLEWVAISGRGNTYY 60
Db 80 EVQLVESGGGLVQSGGSLRLSCVAAGLTFSSTAITWROAPGKLEWVSGISFGDTYY 139
QY 61 ADSVKGRFTISRDNSKNTLYLQNNLSRAEDTAVYYCAKMTSNAFADYWGQGLTVVSS- 119
Db 140 ADSVKGRFASRSRNSKNTLYLQNNLRPNDAVYFCAANNQTFCLDNNQGGTLTVSSR 199
QY 120 GGGSGGGGGGGG--GSQSVLTQPPSVSGAPGQRTVISTCGSSSNIGAGYVHWYQQLPG 177
Db 200 GGGSGGGGGGGGSSQSVLTQPPSVSAAPGQRTVISTCGSSSNIGAGYVHWYQKFP 259
QY 178 TAPKLIYGNTRPSGVPRFSGFGKSGTSASLAITGLQADEADYVCOFYDSSLGWFV 237
Db 260 TAPKLIYNNNRPSGVPRFSGFGKSGTSASLAITGLQDEBETYYCQCNDSSLGWLFG 319
QY 238 GGTKLTVL 245
Db 320 GGTKLTVL 327

RESULT 3
US-09-646-028-55
; Sequence 55, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsayn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
```

```
; TITLE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 55
; LENGTH: 339
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-55

Query Match 78.3%; Score 1017.5; DB 4; Length 339;
Best Local Similarity 79.8%; Pred. No. 1.2e-70;
Matches 198; Conservative 13; Mismatches 34; Indels 3; Gaps 2;

QY 1 QVOLVESGGGLVOPGGSLRLSCAASGFTPRSYAMSWVROAPGKLEWVAISGRGNTYY 60
Db 85 EVQLVESGGGLVQSGGSLRLSCVAAGLTFSSTAITWROAPGKLEWVSGISFGDTYY 144
QY 61 ADSVKGRFTISRDNSKNTLYLQNNLSRAEDTAVYYCAKMTSNAFADYWGQGLTVVSS- 119
Db 145 ADSVKGRFASRSRNSKNTLYLQNNLRPNDAVYFCAANNQTFCLDNNQGGTLTVSSR 204
QY 120 GGGSGGGGGGGG--GSQSVLTQPPSVSGAPGQRTVISTCGSSSNIGAGYVHWYQQLPG 177
Db 205 GGGSGGGGGGGGSSQSVLTQPPSVSAAPGQRTVISTCGSSSNIGAGYVHWYQKFP 264
QY 178 TAPKLIYGNTRPSGVPRFSGFGKSGTSASLAITGLQADEADYVCOFYDSSLGWFV 237
Db 265 TAPKLIYNNNRPSGVPRFSGFGKSGTSASLAITGLQDEBETYYCQCNDSSLGWLFG 324
QY 238 GGTKLTVL 245
Db 325 GGTKLTVL 332

RESULT 4
US-09-646-028-51
; Sequence 51, Application US/09646028
; Patent No. 6562347
; GENERAL INFORMATION:
; APPLICANT: Kwak, Larry
; APPLICANT: Birsayn, Arya
; TITLE OF INVENTION: METHODS AND COMPOSITIONS OF
; FILE OF INVENTION: CHEMOKINE-TUMOR ANTIGEN FUSION PROTEINS AS CANCER VACCINES
; FILE REFERENCE: 14014.0316/P
; CURRENT APPLICATION NUMBER: US/09/646,028
; CURRENT FILING DATE: 2000-09-12
; PRIOR APPLICATION NUMBER: 60/077,745
; PRIOR FILING DATE: 1998-03-12
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 51
; LENGTH: 348
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of artificial sequence:/note=synthetic construct
US-09-646-028-51

Query Match 78.3%; Score 1017.5; DB 4; Length 348;
Best Local Similarity 79.8%; Pred. No. 1.2e-70;
Matches 198; Conservative 13; Mismatches 34; Indels 3; Gaps 2;

QY 1 QVOLVESGGGLVOPGGSLRLSCAASGFTPRSYAMSWVROAPGKLEWVAISGRGNTYY 60
Db 94 EVQLVESGGGLVQSGGSLRLSCVAAGLTFSSTAITWROAPGKLEWVSGISFGDTYY 153
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```

0Y 6L ADSVGRFPIASDNSKNTLYLOMNS:RAEDTAYVCARKMTSNAFAPYMOGGLTWYSS- 119
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 154 ADSVGRFSASDNSKNTLYLOMNI:RPMDTAVYFCANNOTGFGFCLDMOGGLTWYSSR 213
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0Y 120 GGGGSGGGSGGG--GSQSVLTQPPSVSGAPGQRTVTSCTGSSSNTGAGYGVHMYQGLPG 177
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 214 GGGGSGGGSGGGSGGSQSVLTQPPSVSNAAPGQRTVTSCTGSSSNTGAGYGVHMYQGFPE 273
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0Y 178 TAPKLLIYGNTRPFSVPDRFSGFKSGTASLAITGLQAEDEADYYCQFIDSLSGVFG 237
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 274 TAPKLLIYNNNRPFSGVDRFSGSKSGTASLAITGLQAEDEBETYYCQCDNDLSGLFG 333
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
0Y 238 GGTXLTVL 245
    |||:|||||
Db 334 GGTXLTVL 341
    |||:|||||

```

RESULT 5
US-09-07

; Sequence 10, Application US/09079029
; Patent No. 6342369
CHUNMAI INFORMATION

;
; GENERAL INFORMATION:
;
; APPLICANT: Adams,
;

```

;
;  APPLICANT: Ashkenazi, Avi J.
;
;  APPLICANT: Chuntcharapai, Anan
;
;  APPLICANT: Kim, Kyung J.
;
;  TITLE OF INVENTION: Apo-2 Receptor
;
;  NUMBER OF SEQUENCES: 14
;

```

```

CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-10

Query Match          68.7%; Score 892.5; DB 3; Length 312;
Best Local Similarity 72.8%; Pred. No. 4,3e-61;
Matches 182; Conservative 13; Mismatches 46; Indels 9; Gaps 3

2 VOLVESGGGLVOPGSLRLSCAASGFTFRSYAMSWRQAPFKGLEWVSAISGRGNTYYA 61
41 VOLVESGGGLVOPGSGSLRLSCAASGFTFRSYAMSWRQAPFKGLEWVSAISKOGSEKYYV 100
62 DSVKRGFTISRDNSKNTLYIOMNSLAEDTAVYYCAK-----MTSNAPFDYWGQGLT 116
101 DSVKRGFTISRDARNSLYIOMNSLAEDTAVYYCARDLTKVGSSEGWFDPMRGITVT 160
117 VSSGGGSGGGGSGGGGSSVLTQPSVSGAPGQRYTISCTGSSSNIGAGYGVHWYQQLP 176
161 VSSGGGSGGGGSGGGGSS-SELTDPAVSVVAGQTWRITCGDPSLR---SYASWYQKP 216

```

[illegible]

RESULT 6
US-09-07

; Sequence 9, Application US/09079029
; Patent No. 6342369
GENERAL INFORMATION.

GENEACD INFORMATION:
APPLICANT: Adams, Camilla W.
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Chuncharapai, Anan
APPLICANT: Kim, Kyung J.
TITLE OF INVENTION: Abo-2 Receptor

NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco

```

STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,029
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Marschang, Diane L.
REGISTRATION NUMBER: 35,600
REFERENCE/DOCKET NUMBER: P1101R2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-5416
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-079-029-9

Query Match      68.2%; Score 887; DB 3; Length 309;
Best Local Similarity 71.8%; Pred. No. 1,1e-60;
Matches 178; Conservative 17; Mismatches 47; Indels 6; Gaps 3;

OY    1 QVQLVESGGGLVPGSSLRISCAASGTFPFSYAMSWVRQAPKGKLEWVSATSGRDITY 60
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB    40 EVQLVDSGGGVGERPGSLSRLSCAASGTFDPYGMSWRQAPKGKLEWVSGINMGSGSYG 99
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

OY    61 ADSVKGFPTISRDSKNTLYLQNMSLAEDPAVYYCAKM--TSNAFAFDYWGQTLTVTS 118
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB    100 ADSVKGRVTISRDAKNSLYIQNMSLAEDPAVYYCAKIIGAGGWYFDLMGKTITVTS 159
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

OY    119 SGGSGSGSGSGSGGSQSIVLTQPPSVSGAPQRVTISCSSSNIGAGYGVHWYQOLPET 178
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB    160 SGGGSGSGSGSGSGGS--SELTQDPAVSVALGQTVIRITCGGSLR---SYNASWYQKRGQ 215
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

OY    179 APKLTIYGNTPRPBGVDPRPSGFGSSGTSAIATGLAEADPADYYCQFYVSSLGWFEG 238
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
DB    216 APVLVIYIGNKNRPBGILPDPRSGSSGNVTASLTITGAQDEADYYCNRSDDSGNHVFGG 275
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

OY    239 GTKLTVLG 246
       |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||

```



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Query Match Similarity      64.7% Score 841.5: DB 3 Length 281;
Best Local Similarity      68.8%; Pred No. 3,2e-57;
Matches 174; Conservative 23; Mismatches 45; Indels 11; Gaps 6

QY      1 QVQLVESGGGLVQPGGSLRLSCAASGFTFRSYAMSWVRQAPKGLEWVSATISGRGNTYY 60
Db      26 EVQLVESGGGLVQPGGSLRLSCAASGFTFRSYAMSWVRQAPKGLEWVSATISGGSGSTYY 85
QY      61 ADVYKGRFTISRDNSKNTLYIQMNSLRADDTAVYCAKMTSNAF AFDYWGQGTLLVTVS 118
Db      86 ADVYKGRFTISRDNSKNTLYIQMNSLRADDTAVYCAKMGSGGFFYAMDYWGQGTLLVTVS 145
QY      119 ----SGGGSGGGGGSGGGSGQSVLTROP-SVSGAPGQQRVTISCTGSSSNIGA-GYG-VHM 171
Db      146 AGGGSGGGGGSGGGSGGGGGSDIVMTQSPILSTLVTEGEPASISCRSGQSLHNGNYIYDM 205
QY      172 YQQLFPTAPKLLIYGNTPRPGVDPDRFSGFKSGTSASLAITGLQAEDEADYICQFYDSL 231
Db      206 YLQKPGQSPQLLIYGNTPRPGVDPDRFSGSGGTDFTLKISRVEAEDVGVYCOQHYYTP 265
QY      232 SGWVFGGSKLTIV 244
Db      266 P-ITGGGTKEI 276

RESULT 12
US-09-490-070A-178
Sequence 178, Application US/09490070A
Patent No. 6696248
GENERAL INFORMATION:
APPLICANT: Knappik, Achim
Pack, Peter
Ilag, Vic
Ge, Liming
Moroney, Simon
Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly)peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/490,070A
FILING DATE: 24-Jan-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Colin G. Sandercock, Esq.
REGISTRATION NUMBER: 31,298
REFERENCE/DOCKET NUMBER: 37629-0005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 912-2000
TELEFAX: (202) 912-2020
INFORMATION FOR SEQ ID NO: 178:
SEQUENCE CHARACTERISTICS:
LENGTH: 281 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 178:
US-09-490-070A-178

```

	Query Match	64.7%	Score 841.5	DB 3	Length 281
	Best Local Similarity	68.8%	Pred. No. 3.2e-57		
	Matches	174	Conservative	23	Mismatches 45; Indels 11; Gaps 6
QY	1 QVQLVESGGGLVQPFGSLRLSCAASGFTFRSAMSWMVRCAPEKGLEWNSAISGRGNITY	60	:	:	:
Dd	26 EVQLVESGGGLVQPFGSLRLSCAAGFTFSSVAMSWVRCAPEKGLEWNSAISGSGSTYY	85	:	:	:
QY	61 ADSVKGRFTTISHDNSKNTLYIQMNSLRAEDTAVVYCAKMTSNAF-AFDYWGCGTLTVTS-	118	:	:	:
Dd	86 ADSVKGRTTISHDNSKNTLYIQMNSLRADDTAVVYCARVGDDGFAYMDYWGCTLVTVSS	145	:	:	:
QY	119 -----SGGGSGGGGGSGGSQSIVLTQPP-SVSGAQQRATICTGSSNIIGA-GYG-VHM	171	:	:	:
Dd	146 AGGGGGGGGGSGGGGGSDIWMVQSPISLTVPDEPASIICRSQSIILHNSGVNYLDW	205	:	:	:
QY	172 YQQLPGTAKLLTYENTNRPSGVPRFSGFKSQTASALITGLQAEDEADYYCQPFDSL	231	:	:	:
Dd	206 YLQRPDGPQLLIYIGSNRNASVPDRFSGSGSDTFLLTKISRVEADVGVYTCQQQHYP	265	:	:	:
QY	232 SGWVFGGGTKLTV	244	:	:	:
Dd	266 P--TFPGGTKEYEI	276	:	:	:

```

1      RESULT 12
2      US-09-490-070A-178
3      : Sequence 178. Application US/09490070A
4      : Patent No. 6696248
5      :
6      : GENERAL INFORMATION:
7      :
8      : APPLICANT: Knappik, Achim
9      :           Pack, Peter
10     :           Ilag, Vic
11     :           Ge, Liming
12     :           Moroney, Simon
13     :           Plueckthun, Andreas
14     :
15     : TITLE OF INVENTION: Protein/(Poly)peptide libraries
16     :
17     : NUMBER OF SEQUENCES: 373
18     :
19     : CORRESPONDENCE ADDRESS:
20     :
21     : ADDRESSEE: Colin G. Sandercock, Esq. c/o Heller Ehrman
22     :
23     : STREET: 1666 K Street, N.W., Suite 300
24     :
25     : CITY: Washington
26     :
27     : STATE: D.C.
28     :
29     : COUNTRY: USA
30     :
31     : ZIP: 20006
32     :
33     : COMPUTER READABLE FORM:
34     :
35     : MEDIUM TYPE: Floppy disk
36     :
37     : COMPUTER: IBM PC compatible
38     :
39     : OPERATING SYSTEM: PC-DOS/MS-DOS
40     :
41     : SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
42     :
43     : CURRENT APPLICATION DATA:
44     :
45     : APPLICATION NUMBER: US/09/490,070A
46     :
47     : FILING DATE: 24-Jan-2000
48     :
49     : PRIOR APPLICATION NUMBER: EP 95 11 3021.0
50     :
51     : APPLICATION NUMBER:
52     :
53     : FILING DATE: 18-AUG-1995
54     :
55     : ATTORNEY/AGENT INFORMATION:
56     :
57     : NAME: Colin G. Sandercock, Esq.
58     :
59     : REGISTRATION NUMBER: 31,298
60     :
61     : TELECOMMUNICATION INFORMATION:
62     :
63     : TELEPHONE: (202) 912-2000
64     :
65     : TELEFAX: (202) 912-2020
66     :
67     : INFORMATION FOR SEQ ID NO: 178:
68     :
69     : SEQUENCE CHARACTERISTICS:
70     :
71     : LENGTH: 281 amino acids
72     :
73     : TYPE: amino acid
74     :
75     : TOPOLOGY: linear
76     :
77     : MOLECULE TYPE: protein
78     :
79     : SEQUENCE DESCRIPTION: SEQ ID NO: 178:
80     :
81     : US-09-490-070A-178

```

[illegible]

RESULT 13
 US-09-490-153-178
 ; Sequence 178, Application US/09490153
 ; Patent No. 6706484
 GENERAL INFORMATION:
 APPLICANT: Knappik, Achim
 Pack, Peter
 Illig, Vic
 Ge, Liming
 Moroney, Simon
 Plueckhnn, Andreas
 TITLE OF INVENTION: Protein/(poly)peptide libraries
 NUMBER OF SEQUENCES: 373
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave
 STREET: 1251 Avenue of the Americas
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10021
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/490,153
 FILING DATE: 24-Jan-2000
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US/09/025,769B
 FILING DATE: 18-FEB-1998
 APPLICATION NUMBER: EP 95 11 3021.0
 FILING DATE: 18-AUG-1995
 ATTORNEY/AGENT INFORMATION:
 NAME: James F. Haley, Jr., Esq.
 REGISTRATION NUMBER: 27,794
 REFERENCE/DOCKET NUMBER: MORPHO/5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212)596-9000
 TELEFAX: (212)596-9090
 INFORMATION FOR SEQ ID NO: 178:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 281 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 178:
 US-09-490-153-178

Db :||| |||:||||
237 PYVFGTGTAVIG 250

Search completed: April 19, 2005, 16:45:19
Job time : 31.2459 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: April 19, 2005, 16:43:24 ; Search time 88.7213 Seconds
(without alignments)
921.573 Million cell updates/sec

Title: US-09-250-056B-1

Perfect score: 1300
Sequence: 1 QVQLVESGGGLVQPGGSLRL.....YDSLSGWMVFGGCTKLTIVIG 246

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA.*
1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1300	100.0	246	17	US-10-855-755-1
2	1292	99.4	291	15	US-10-406-830-1
3	1292	99.4	291	15	US-10-406-830-2
4	1135.5	87.3	245	16	US-10-779-461-59
5	1125.5	86.6	247	10	US-09-880-748-1892
6	1125.5	86.6	247	15	US-10-293-418-1892
7	1121.5	86.3	258	16	US-10-688-925-20
8	1113.5	85.7	247	10	US-09-880-748-1978
9	1113.5	85.7	247	15	US-10-293-418-1978
10	1096.5	84.3	258	16	US-10-688-925-8
11	1092.5	84.0	247	10	US-09-880-748-1953
12	1092.5	84.0	247	15	US-10-293-418-1953
13	1092	84.0	252	10	US-09-880-748-1519

14	1092	84.0	252	15	US-10-293-418-1519	Sequence 1519, Ap
15	1084	83.4	228	16	US-10-779-461-1	Sequence 1, Appl
16	1081	83.2	252	10	US-09-880-748-1362	Sequence 1362, Ap
17	1081	83.2	252	15	US-10-293-418-1362	Sequence 1362, Ap
18	1080	83.1	258	10	US-09-880-748-1841	Sequence 1841, Ap
19	1080	83.1	258	15	US-10-293-418-1841	Sequence 1841, Ap
20	1076.5	82.8	243	10	US-09-880-748-1969	Sequence 1969, Ap
21	1076.5	82.8	243	15	US-10-293-418-1969	Sequence 1969, Ap
22	1075.5	82.7	310	13	US-10-052-798-11	Sequence 11, Appl
23	1075.5	82.7	310	14	US-10-288-917-11	Sequence 11, Appl
24	1075.5	82.7	310	15	US-10-423-448-11	Sequence 11, Appl
25	1069	82.2	252	10	US-09-880-748-1201	Sequence 1201, Ap
26	1069	82.2	252	15	US-10-293-418-1201	Sequence 1201, Ap
27	1065.5	82.0	262	16	US-10-688-925-2	Sequence 2, Appl
28	1062	81.7	250	10	US-09-880-748-1420	Sequence 1420, Ap
29	1062	81.7	250	15	US-10-293-418-1420	Sequence 1420, Ap
30	1059.5	81.5	253	14	US-10-120-414-76	Sequence 76, Appl
31	1056	81.2	246	14	US-10-120-414-80	Sequence 80, Appl
32	1053.5	81.0	243	16	US-10-779-461-46	Sequence 46, Appl
33	1048	80.6	250	10	US-09-880-748-1461	Sequence 1461, Ap
34	1048	80.6	250	15	US-10-293-418-1461	Sequence 1461, Ap
35	1045	80.4	246	16	US-10-779-461-45	Sequence 45, Appl
36	1045	80.4	246	16	US-10-779-461-47	Sequence 47, Appl
37	1044.5	80.3	245	16	US-10-779-461-24	Sequence 24, Appl
38	1044	80.3	248	10	US-09-880-748-1890	Sequence 1890, Ap
39	1044	80.3	248	15	US-10-293-418-1890	Sequence 1890, Ap
40	1043	80.2	240	10	US-09-880-748-1905	Sequence 1905, Ap
41	1043	80.2	240	15	US-10-293-418-1905	Sequence 1905, Ap
42	1040.5	80.0	243	14	US-10-322-673-51	Sequence 51, Appl
43	1039	79.9	240	10	US-09-880-748-2016	Sequence 2016, Ap
44	1039	79.9	240	15	US-10-293-418-2016	Sequence 2016, Ap
45	1039	79.9	260	10	US-09-880-748-1458	Sequence 1458, Ap

ALIGNMENTS

RESULT 1
US-10-855-755-1
Sequence 1, Application US/10855755
Publication No. US20050037339A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Marks, James D
APPLICANT: Poul, Marie A
TITLE OF INVENTION: METHODS OF SELECTING INTERNALIZING ANTIBODIES
FILE REFERENCE: 4070-895011US
CURRENT APPLICATION NUMBER: US/10/855,755
CURRENT FILING DATE: 2004-05-26
PRIOR APPLICATION NUMBER: US 60/082,953
PRIOR FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 246
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Human phage display antibody
NAME/KEY: SITE
LOCATION: (31)..(35)
OTHER INFORMATION: VH-CDR1
NAME/KEY: SITE
LOCATION: (50)..(66)
OTHER INFORMATION: VH-CDR2
NAME/KEY: SITE
LOCATION: (99)..(108)
OTHER INFORMATION: VH-CDR3
FEATURE:

NAME/KEY: SITE
LOCATION: (157)..(170)
OTHER INFORMATION: VL-CDR1
FEATURE:
NAME/KEY: SITE
LOCATION: (186)..(192)
OTHER INFORMATION: VL-CDR2
FEATURE:
NAME/KEY: SITE
LOCATION: (225)..(235)
OTHER INFORMATION: VL-CDR3
US-10-855-755-1

Query Match 100.0%; Score 1300; DB 17; Length 246;
Best Local Similarity 100.0%; Pred. No. 7.8e-81;
Matches 246; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQVSEGGGLVQPGGSLRLSCAAGFTFRSYAMSWVRQAPGKLEWVAISGRGNTYY 60
DB 1 QVQVSEGGGLVQPGGSLRLSCAAGFTFRSYAMSWVRQAPGKLEWVAISGRGNTYY 60
QY 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120
DB 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120
QY 121 GGGSGGGSGGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYVHWYQQLPGTAP 180
DB 121 GGGSGGGSGGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYVHWYQQLPGTAP 180
QY 181 KLLIYGNTRPSGVDPDRFSGFGKTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGGT 240
DB 181 KLLIYGNTRPSGVDPDRFSGFGKTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGGT 240
QY 241 KLTVLG 246
DB 241 KLTVLG 246

RESULT 2

US-10-406-830-1
Sequence 1, Application US/10406830
Publication No. US20040071696A1
GENERAL INFORMATION:
APPLICANT: ADAMS, GREGORY P.
APPLICANT: HORAK, EVA M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: JAMES, MARKS D.
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
FILE REFERENCE: 407T-000410US
CURRENT APPLICATION NUMBER: US/10/406,830
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,276
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 291
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic antibody.
US-10-406-830-1

Query Match 99.4%; Score 1292; DB 15; Length 291;
Best Local Similarity 99.6%; Pred. No. 3.2e-80;
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQVSEGGGLVQPGGSLRLSCAAGFTFRSYAMSWVRQAPGKLEWVAISGRGNTYY 60
DB 23 QVQVSEGGGLVQPGGSLRLSCAAGFTFRSYAMSWVRQAPGKLEWVAISGRGNTYY 82
QY 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120

DB 83 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 142
QY 121 GGGSGGGSGGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYVHWYQQLPGTAP 180
DB 143 GGGSGGGSGGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYVHWYQQLPGTAP 202
QY 181 KLLIYGNTRPSGVDPDRFSGFGKTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGGT 240
DB 203 KLLIYGNTRPSGVDPDRFSGFGKTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGGT 262
QY 241 KLTVLG 246
DB 263 KLTVLG 268

RESULT 3

US-10-406-830-2
Sequence 2, Application US/10406830
Publication No. US20040071696A1
GENERAL INFORMATION:
APPLICANT: ADAMS, GREGORY P.
APPLICANT: HORAK, EVA M.
APPLICANT: WEINER, LOUIS M.
APPLICANT: JAMES, MARKS D.
TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
FILE REFERENCE: 407T-000410US
CURRENT APPLICATION NUMBER: US/10/406,830
CURRENT FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: US 60/370,276
PRIOR FILING DATE: 2002-04-05
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 291
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic antibody.
US-10-406-830-2

Query Match 99.4%; Score 1292; DB 15; Length 291;
Best Local Similarity 99.6%; Pred. No. 3.2e-80;
Matches 245; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 QVQVSEGGGLVQPGGSLRLSCAAGFTFRSYAMSWVRQAPGKLEWVAISGRGNTYY 60
DB 23 QVQVSEGGGLVQPGGSLRLSCAAGFTFRSYAMSWVRQAPGKLEWVAISGRGNTYY 82
QY 61 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 120
DB 83 ADVKGRFTISRDNKNTLYLQMSLRADDTAVYYCAKMTSNAFAFDYWGQGLTVTVSSG 142
QY 121 GGGSGGGSGGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYVHWYQQLPGTAP 180
DB 143 GGGSGGGSGGGGSGSVLTQPPSVSGAPGQRTVITCTGSSSNIGAGYVHWYQQLPGTAP 202
QY 181 KLLIYGNTRPSGVDPDRFSGFGKTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGGT 240
DB 203 KLLIYGNTRPSGVDPDRFSGFGKTSASLAITGLQAEDEADYYCQFYDSSLGWFVGGGT 262
QY 241 KLTVLG 246
DB 263 KLTVLG 268

RESULT 4

US-10-779-461-59
Sequence 59, Application US/10779461
Publication No. US20040166544A1
GENERAL INFORMATION:
APPLICANT: Morton, Philip A

Db 181 PRLISSNTNRPSSGVDRFSGSKSGTASLAITGLQAEDEADYCCQSYDSSLGTFVFGTG 240

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QY      240 TKLTVLG 246
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Db      241 TKTVLVG 247

RESULT 7
US-10-688-925-20
; Sequence 20, Application US/10688925
; Publication No. US20040142382A1
; GENERAL INFORMATION:
; APPLICANT: Veldman, Geertjida et al.
; TITLE OF INVENTION: NEUTRALIZING ANTIBODIES AGAINST GDF 8 AND USES THEREFOR
; FILE REFERENCE: 08702.0020-00000
; CURRENT APPLICATION NUMBER: US/10/688,925
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 258
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-688-925-20

Query Match      86.3%; Score 1121.5; DB 16; Length 258;
Best Local Similarity 86.3%; Pred. No. 1.1e-68;
Matches 215; Conservative 13; Mismatches 18; Indels 3; Gaps 2;

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Db      1 EVQLVESGGGLVQPGGSLRLSCAASGFTSRVYINMWROAPGKLEWVAISITVGSTAY 60

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAK--MTSNAPFDPYWGQTLTVTS 118
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Db      61 ADSVGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKQGWKRGSYYPDYWGRTLVTS 120

QY      119 SGGSGSGGGSGGGGGS-QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYGVHWYQQLPG 177
      ||:|||||
Db      121 SGGSGSGGGSGGGGSAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGDYDVHWYQQLPG 180

QY      178 TAPKLLIYGNTRPSGVPRFSGFGKSTASLAITGLQAEDEADYYCQFYDSSLGWFVPG 237
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Db      181 TAPKLLIYGNTRPSGVPRFSGSGKSTASLAITGLQAEDEADYYCHSYDSSVSGWITG 240

QY      238 GGTKLTVLG 246
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Db      241 GGTKLTVLG 249

RESULT 8
US-09-880-748-1978
; Sequence 1978, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; NUMBER OF SEQ ID NOS: 247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1978

Query Match      85.7%; Score 1113.5; DB 16; Length 247;
Best Local Similarity 85.8%; Pred. No. 3.7e-68;
Matches 212; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
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QY      1 QVQLVSGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSATISGRGDNITY 60
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Db      1 EVQLVETGGGLVQPGGSLRLSCAASGLTFSSYAMTWVRQAPGKLEWVAISIGNSNTYH 60

QY      61 ADSVKGRFTISRDNKNTLYLQMNSLRAEDTAVYYCAKMTSNAPFDPYWGQTLTVSSG 120
      ||:|||||
Db      61 ADVVGRFTASRDNKNTLYLQMNSLTADDSAVYYCAKGNPKGYFEYWGQGLTVTVSSG 120

QY      121 GGGSGGGGSGGGGGS-QSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYGVHWYQQLPGR 179
      ||:|||||
Db      121 GGGSGGGGSGGGGSAQSVLTQPPSVSGAPGQRVTISCTGSSSNIGAGYDVHWYQQLPRT 180

QY      180 PRLIYGNTRPSGVPRFSGFGKSTASLAITGLQAEDEADYYCQFYDSSLGWFVGGG 239
      ||:|||||
Db      181 PRLIFGNNTNRPSGVPRFSGSGRSVTSASLVITGLQPDDEADYYCQSYDSSLGWFVGGG 240

QY      240 TKLTVLG 246
      ||:||||
Db      241 TKLTVLG 247

RESULT 9
US-10-293-418-1978
; Sequence 1978, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; NUMBER OF SEQ ID NOS: 3247
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1978

Query Match      85.7%; Score 1113.5; DB 15; Length 247;
Best Local Similarity 85.8%; Pred. No. 3.7e-68;
Matches 212; Conservative 14; Mismatches 20; Indels 1; Gaps 1;
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US-09-880-748-1953
Sequence 1953, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16

RESULT 12
 US-10-293-418-1953
 ; Sequence 1953, Application US/10293418
 ; Publication No. US2003022396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruben et al.
 ; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
 ; FILE REFERENCE: PE523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1953
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-1953

Query Match	84.0%;	Score 1092.5;	DB 15;	Length 247;
Best Local Similarity	85.8%;	Pred. No. 9.9e-67;		
Matches 212;	Conservative 10;	Mismatches 24;	Indels 1;	Gaps 1;

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QY 1 QVOLVESGGGLVOPGGSRLSLSCAASGFTFRSYAMSVWRQAPGKLEWVAISGRGNTYY 60
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Db 1 EVOVLVESGGGLVOPGMSLRLSLSCAASGFTFSYAMTWRQAPGKLEWVAISGGATYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNNSLRADDTAVYCAKRTSNAPADYVGGGTLVTVSSG 120
   |||||
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRADDTAVYCAKRTSNAPADYVGGGTLVTVSSG 120
QY 121 GGGSGGGSGGGGS-OSVLTQPPSVGAPGQRTTISCTSSNIGAGYVHWYQQLPGTA 179
   |||||
Db 121 GGGSGGGSGGGGSASQVLTQPPSVGAPGQRTTISCTSSNIGAGYVHWYQQLPGTA 180
QY 180 PKLLIYGNTRPSGVDPDRFSGFKSGTSASLAITGLQAEDEADYVCOFYDSSLGWFVGGG 239
   |||||
Db 181 PKLLIYGNTRPSGVDPDRFSGFKSGTSASLAITGLQAEDEADYVCOFYDSSLGWFVGGG 240
QY 240 TKLTVLG 246
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Db 241 TKLTVLG 247

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RESULT 13
US-09-880-748-1519
; Sequence 1519, Application US/09880748
; Publication No. US20030059937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523
; CURRENT APPLICATION NUMBER: US/09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1519

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Query Match      84.0%; Score 1092; DB 10; Length 252;
Best Local Similarity 84.5%; Pred. No. 1.1e-66;
Matches 213; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 1 QVOLVESGGGLVOPGGSRLSLSCAASGFTFRSYAMSVWRQAPGKLEWVAISGRGNTYY 60
   |||||
Db 1 QVOLVESGGGLVOPGMSLRLSLSCAASGFTFSYAMTWRQAPGKLEWVAISYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNNSLRADDTAVYCAKRTSNAPADYVGGGTLVTVSSG 115
   |||||
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRADDTAVYCAKRTSNAPADYVGGGTLVTVSSG 120
QY 116 TVSSGGSGGGSGGGGS-OSVLTQPPSVGAPGQRTTISCTSSNIGAGYVHWYQQLPGTA 174
   |||||
Db 121 TVSSGGSGGGSGGGGSQAVLTQPPSVGAPGQRTTISCTSSNIGAGYVHWYQQLPGTA 180
QY 175 LPEGTAPKLLIYGNTRPSGVDPDRFSGFKSGTSASLAITGLQAEDEADYVCOFYDSSLG 234
   |||||
Db 181 LPEGTAPKLLIYGNTRPSGVDPDRFSGFKSGTSASLAITGLQAEDEADYVCOFYDSSLG 240
QY 235 VEGGGRKTLTVLG 246
   |||||
Db 241 IFGTGKTVTVLG 252

```

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RESULT 14
US-10-293-418-1519
; Sequence 1519, Application US/10293418
; Publication No. US2003022396A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; PRIOR FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1519
; LENGTH: 252
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1519

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Query Match      84.0%; Score 1092; DB 15; Length 252;
Best Local Similarity 84.5%; Pred. No. 1.1e-66;
Matches 213; Conservative 9; Mismatches 24; Indels 6; Gaps 2;

QY 1 QVOLVESGGGLVOPGGSRLSLSCAASGFTFRSYAMSVWRQAPGKLEWVAISGRGNTYY 60
   |||||
Db 1 QVOLVESGGGLVOPGMSLRLSLSCAASGFTFSYAMTWRQAPGKLEWVAISYDGSNKYY 60
QY 61 ADSVKGRFTISRDNKNTLYLQNNSLRADDTAVYCAKRTSNAPADYVGGGTLVTVSSG 115
   |||||
Db 61 ADSVKGRFTISRDNKNTLYLQNNSLRADDTAVYCAKRTSNAPADYVGGGTLVTVSSG 120
QY 116 TVSSGGSGGGSGGGGS-OSVLTQPPSVGAPGQRTTISCTSSNIGAGYVHWYQQLPGTA 174
   |||||
Db 121 TVSSGGSGGGSGGGGSQAVLTQPPSVGAPGQRTTISCTSSNIGAGYVHWYQQLPGTA 180
QY 175 LPEGTAPKLLIYGNTRPSGVDPDRFSGFKSGTSASLAITGLQAEDEADYVCOFYDSSLG 234
   |||||
Db 181 LPEGTAPKLLIYGNTRPSGVDPDRFSGFKSGTSASLAITGLQAEDEADYVCOFYDSSLG 240
QY 235 VEGGGRKTLTVLG 246
   |||||
Db 241 IFGTGKTVTVLG 252

```

```

RESULT 15
US-10-779-461-1
; Sequence 1, Application US/10779461
; Publication No. US2004016654A1
; GENERAL INFORMATION:
; APPLICANT: Morton, Philip A
; TITLE OF INVENTION: ANTIBODIES TO C-MET FOR THE TREATMENT OF CANCERS
; FILE REFERENCE: 00980/1
; CURRENT APPLICATION NUMBER: US/10/779,461
; PRIOR FILING DATE: 2004-02-13
; PRIOR APPLICATION NUMBER: 60/447,073
; PRIOR FILING DATE: 2003-02-13
; NUMBER OF SEQ ID NOS: 161

```


SOFTWARE: PatentIn version 3.2
SEQ ID NO 1
LENGTH: 238
TYPE: PRT
ORGANISM: artificial
FEATURE:
OTHER INFORMATION: phage display generated human antibody
US-10-779-461-1

Query Match 83.4%; Score 1084; DB 16; Length 238;
Best Local Similarity 86.6%; Pred. No. 3.6e-66;
Matches 214; Conservative 7; Mismatches 14; Indels 12; Gaps 3;
QY 1 QVQLVESGGGLVQPGRSLRLSCAASGFTFRSYAMSWVRQAPGKLEWVSATISGRGNTYY 60
1 EVQLLESGRGLVQPGSLRLSCAASGFTFSYAMSWVRQAPGKLEWVSATISGSGSTYY 60
QY 61 ADSVKGRFTISRDNSTLTLYLQMSLRADDTAVYYCAR-----WGQGTTVTVSSG 120
61 ADSVKGRFTISRDNSTLTLYLQMSLRADDTAVYYCAR-----WGQGTTVTVSSG 110
DB 121 GGGSGGGSGGGSGS-OSVLTQPPSVGAPGQRTISCTGSSSNIGAGYGVHWYQQLPGTA 179
111 GGGSGGGSGGGSGAQAVALTPSSVSGAPGQRTISCTGSSSNIGADYDHWYQQLPGTA 170
QY 180 PKLLIYGNTRPSPGVDPDFSGFKGTASLAITGLQAEDEADYYCOFYDSLSGM-VFGG 238
171 PKLLIYGNTRPSPGVDPDFSGFKGTASLAITGLQAEDEADYYCOFYDSLSGM-VFGG 230
QY 239 GTKLTVL 245
231 GTKLTVL 237
DB

Search completed: April 19, 2005, 17:00:52
Job time : 90.7213 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 16:32:07 / Search time 27.7254 Seconds
(without alignments)
853.705 Million cell updates/sec

Title: US-09-250-056B-1

Perfect score: 1300

Sequence: 1 QVQLVESGGGLVQPQGSURL.....YDSLSGWMFGGKTLTVLG 246

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	612	47.1	268	2 A56446	Ig heavy chain V r
2	611.5	47.0	249	2 S41374	single chain Fv an
3	556	42.8	119	2 S31107	Ig heavy chain - h
4	554.5	42.7	233	2 JCS322	p53 specific singl
5	548	42.2	119	2 C36005	Ig heavy chain V r
6	546	42.0	119	2 S31108	Ig heavy chain - h
7	545.5	42.0	111	2 S36274	Ig lambda chain V
8	542	41.7	140	2 S31588	Ig heavy chain V r
9	541	41.6	138	2 S31666	Ig heavy chain V r
10	540	41.6	140	2 S31686	Ig heavy chain V r
11	540	41.5	119	2 D36005	Ig heavy chain V r
12	540	41.5	123	2 S31114	Ig heavy chain - h
13	539	41.5	127	2 S38489	Ig heavy chain - h
14	538.5	41.4	124	2 S20782	Ig heavy chain V r
15	537	41.3	112	2 S51148	antibody light cha
16	531.5	40.9	120	2 S48798	Ig heavy chain V r
17	529	40.7	160	2 S05271	Ig heavy chain pre
18	526	40.5	121	2 I55673	Ig heavy chain - h
19	523	40.2	135	2 S31598	Ig heavy chain V r
20	521	40.1	236	2 S25746	Ig lambda chain -
21	520	40.0	134	2 S31699	Ig heavy chain V r
22	513	39.5	119	2 F36005	Ig heavy chain V r
23	511.5	39.4	120	2 S36278	Ig heavy chain V r
24	510.5	39.3	140	2 S70442	Ig heavy chain pre
25	510.5	39.3	112	2 S31447	Ig heavy chain V r
26	508	39.1	121	2 S19666	Ig heavy chain V r
27	508	39.1	121	2 G36005	Ig heavy chain V r
28	507.5	39.0	133	2 S31510	Ig heavy chain - h
29	507	39.0	109	2 PH1649	Ig heavy chain V r

30	507	39.0	132	2 S31603	Ig heavy chain V r
31	507	39.0	134	2 S31679	Ig heavy chain V r
32	504.5	38.8	216	2 S29258	Ig lambda chain V
33	503.5	38.7	120	2 S31112	Ig heavy chain - h
34	502.5	38.7	114	2 S31120	Ig heavy chain - h
35	502.5	38.7	118	2 S31116	Ig heavy chain - h
36	502.5	38.7	120	2 S44111	Ig heavy chain V-D
37	502.5	38.7	151	2 A60943	Ig heavy chain pre
38	502	38.6	121	2 S31113	Ig heavy chain - h
39	502	38.6	125	2 S30531	Ig heavy chain V r
40	501.5	38.6	143	2 S23624	Ig heavy chain V r
41	501	38.5	217	2 UE0246	Ig lambda chain NI
42	500.5	38.5	114	2 S46390	Ig heavy chain V r
43	500.5	38.5	122	2 S31117	Ig heavy chain V r
44	499.5	38.4	108	2 PH1648	Ig heavy chain V r
45	498.5	38.3	137	2 S31701	Ig heavy chain V r

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)
C/Species: Mus musculus (house mouse)
C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
C/Accession: A56446
R/Tang, P.M.; Poltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally identical to the

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TRAN>

A/Cross-references: GB:U20617

C/Keywords: heterotrimer; immunoglobulin

Query Match 47.1%; Score 612; DB 2; Length 268;

Best Local Similarity 51.2%; Pred. No. 8.2e-34;

Matches 126; Conservative 35; Mismatches 75; Indels 10; Gaps 5;

QY	1 QVQLVESGGGLVQPQGSURLSCAASGFTFRSYAMSWRQAPKGLLEWVAISRGDNTYY 60	
DB	3 QVQLVESGGGLVQPQGSURLSCAASGFTFRSYAMSWRQAPKGLLEWVAISRGDNTYY 62	
QY	61 ADSVKGRFTISRDNSKNTLYIQMNSLRADIVYVYCAKMTSNAPAFDYGGGLTVVSSG 120	
DB	63 DKPFGKATIAADTSNTAYLQLSSITSEDIAYVYCAASYLTRYE-NWGGGTTVVSSG 121	
QY	121 GGGSGGGSGGGGGSGSGLVLPQPSV--SGAPGQRVTISCTGSSS-NIGAGYGVHMYOQLPGT 178	
DB	122 GGGSGGGSGGGGGSGSGLVLPQPSV--SGAPGQRVTISCTGSSS-NIGAGYGVHMYOQLPGT 176	
QY	179 APKLIVGNTNRPSPGDFRFGSKGTSASLAITGLQADEADYVYCOFYDSSLSGWFPG 238	
DB	177 SKLWVYVYSHLPQGVPAFSSGSGNSYSLTSSMEGDAITVYVYQQTSS--SPTFSS 234	
QY	239 GTKLTV 244	
DB	235 GTKLTV 240	

RESULT 2

S41374
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Artezenko, O.; Weller, E.W.; Muentz, K.; Conrad, U.

Submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibody

A/Reference number: S41374


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QY      1 QVQLVESGGGLVQPGGSLRLSCAAGFTRFSYAMSWVROAPGKLEWWSAISGRGNTYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      1 EVQLLESGGGLVQPGGSLRLSCAAGFTRFSYAMSWVROAPGKLEWWSAISGRGNTYY 60
      :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      61 ADSVNGRFTISRDNKNTLYLQWNSLRADPTAVYYCAKMTSNFA-----FDYWGQGLV 115
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      61 ADSVNGRFTISRDNKNTLYLQWNSLRADPTAVYYCAKRIALFGVVIPIPHFDYWGQGLV 120
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      116 TVSS 119
      |||||
Db      121 TVSS 124

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RESULT 15

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S51148
antibody light chain V region - human (fragment)
C/Species: homo sapiens (man)
C/Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C/Accession: S51148
R/de Krulif, J.; Boel, E.; Logtenberg, T.
submitted to the EMBL Data Library, January 1995
A/Description: Selection and application of human SCFV antibody fragments from a semi-sy
A/Reference number: S51147
A/Accession: S51148
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-112 <DEK>
A/Cross-references: UNIPROT:Q8WUK4; EMBL:X63713
C/Superfamily: immunoglobulin V region; immunoglobulin homology
F:13-90/Domain: immunoglobulin homology <IMM>

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Query Match      41.3%; Score 537; DB 2; Length 112;
Best Local Similarity 94.5%; Pred. No. 3.3e-29;
Matches 103; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY      138 LTQPPSVSGAPGQRTVISTCTGSSSNIAGAGVHWYQQLPGTAPKLIYGNTRRPSGVDPDR 197
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      2 LTQPPSVSGAPGQRTVISTCTGSSSNIAGAGVHWYQQLPGTAPKLIYGNTRRPSGVDPDR 61
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
QY      198 FSGFKSGTASLAITGLQABDEADYYCOFYDSLSGWFVGGGTKLTVLG 246
      |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db      62 FSGSKSGTASLAITGLQABDEADYYCOSYDSLSGSAFPGGTKLTVLG 110

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Search completed: April 19, 2005, 16:44:12
 Job time : 28.7254 secs

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Db 234 TKLEI 238

RESULT 2

06KB05 PRELIMINARY; PRT; 255 AA.

ID 06KB05

AC 06KB05

DT 05-JUL-2004 (TREMblrel. 27, Created)

DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)

DE SCFV B8E5 protein (Fragment).

GN Name=SCFV B8E5.

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=Balb/c;

RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,

RA Briand J.P., Hoebeke J.;

RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AJ746180; CAG34081.1; -.

DR HSSP; P01837; IKCR.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_V.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 2.

DR PROSITE; PSS0835; IG_LIKE; 2.

FT NON TER 1

SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DF713B CRC64;

Query Match 59.3%; Score 771; DB 2; Length 255;

Best Local Similarity 62.5%; Pred. No. 2, 1e-46;

Matches 157; Conservative 31; Mismatches 53; Indels 10; Gaps 6;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVSATISGRGNTYY 60

DB 1 QVQLQSGGDLVPGGSLKVSCAASGFTSSYGMWVRQTPDKLEWVAITISGGSYTY 60

QY 61 ADSVGRFTISRDNKNTIYLQNSLRADTAVYYCAKMTSNAP--AFPIYWGQTLTVTS 118

DB 61 PSVVGKRFITSRDNKNTIYLQNSLRADTAVYYCAKMTSNAP--AFPIYWGQTLTVTS 120

QY 119 SGSGSGSGSGSGSGSGSVLTQ--PPEVSGAPGQRTISCTGSSNNIGA---GYGVHWYQ 173

DB 121 SGSGSGSGSGSGSGSGSDIYMAQSPSLYSAGEKVTMSCKSSQSLNSKQNY-LAWYQ 179

QY 174 QLPGTAPKLLIYGNTNRPSPGVPDRFSGFKSGTSASIAITGLQAEDEADYYCFYDSSLG 233

DB 180 QKPGQSPKLLIYGASRRESGVDRFRTGSGSGTDFTLTISVQAEADLAVYYCQ-NDRSYD- 237

QY 234 WYFGGSGTKTV 244

DB 238 LTFGAGTKLEI 248

RESULT 3

06S207 PRELIMINARY; PRT; 248 AA.

ID 06S207

AC 06S207

DT 25-OCT-2004 (TREMblrel. 28, Created)

DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)

DE B3 (Fv) -PE40 (Fragment).

GN Name=B3 (Fv)-PE40;

OS Mus sp.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10095;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=92020904; PubMed=1924323;

RA Brinkmann U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.;

RT "B3 (Fv)-PE38KDEL, a single-chain immunotoxin that causes complete regression of a human carcinoma in mice."

RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620 (1991).

DR EMBL; S57930; AAB1971.2; -.

DR InterPro; IPR003599; Ig.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_V.

DR Pfam; PF00047; IG; 2.

DR SMART; SM00409; IG; 2.

DR SMART; SM00406; IG; 2.

DR PROSITE; PSS0835; IG_LIKE; 2.

FT NON TER 248

SQ SEQUENCE 248 AA; 26634 MW; 7A359BA3E570950 CRC64;

Query Match 54.4%; Score 707.5; DB 2; Length 248;

Best Local Similarity 59.7%; Pred. No. 5, 8e-42;

Matches 148; Conservative 30; Mismatches 61; Indels 9; Gaps 5;

QY 2 VOLVESGGGLVPGGSLRLSCAASGFTPRSYAMSWRQAPGKLEWVSATISGRGNTYYA 61

DB 3 VLVESGGGLVPGGSLKLSGATSGFTSDIYMWVRQTPDKLEWVAISNDSSAAYS 62

QY 62 DSVKGRFTISRDNKNTIYLQNSLRADTAVYYCAKMTSNAPAFDYGQTLTVSSG 121

DB 63 DTVKGRFTISRDNKNTIYLQNSLRADTAVYYCAKMTSNAPAFDYGQTLTVSSG 122

QY 122 GSGSGSGSGSGSGSVLTQPP--SVSGAPGQRTISCTGSS---SNIGAGVHWYQQLP 176

DB 123 GSGSGSGSGSGSVLTQSPSLPSLSDQDSISCRSQIIVHSN-GNTY-LHWYQQLP 180

QY 177 GAPKLLIYGNTNRPSPGVPDRFSGFKSGTSASIAITGLQAEDEADYYCFYDSSLGWF 236

DB 181 GQSPKLLIYKYSNRSVGPDRFSGSGSGTDFTLKISRVEADLGVYYC--FGSHVPTFF 238

QY 237 GGGTYLTV 244

DB 239 GSGTKLEI 246

RESULT 4

09QYF0 PRELIMINARY; PRT; 298 AA.

ID 09QYF0

AC 09QYF0

DT 01-MAY-2000 (TREMblrel. 13, Created)

DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)

DT 01-OCT-2003 (TREMblrel. 25, Last annotation update)

DE CN 8 single chain antibody.

GN Name=CN 8 scFv;

OS synthetic construct.

OC other sequences; artificial sequences.

OX NCBI_TaxID=32630;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;

RA Shinohara N., Demura T., Fukuda H.;

RT "Isolation of a vascular cell wall-specific monoclonal antibody recognizing a cell polarity by using a phage display subtraction method."

RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).

DR EMBL; AB036341; BAA88633.1; -.

DR PIR; A33933; A33933.

DR PIR; S19112; S19112.

DR HSSP; P01820; IATQ.

DR InterPro; IPR007110; Ig-like.

DR InterPro; IPR003596; Ig_V.

DR SMART; SM00406; IG; 2.

DR PROSITE; PSS0835; IG_LIKE; 2.

SQ SEQUENCE 298 AA; 31867 MW; E0F96B8A17004317 CRC64;

Query Match 52.7%; Score 685.5; DB 2; Length 298;

Best Local Similarity 56.2%; Pred. No. 2, 4e-40;

[illegible]

QY	238	GCTKLTV 244
DB	236	GCTKLEI 242

RESULT 6		
ID	Q7TQM2	PRELIMINARY; PRT; 243 AA.
AC	Q7TQM2	01-OCT-2003 (TREMBlrel. 25, Created)
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)
DT	01-OCT-2003	(TREMBlrel. 25, Last sequence update)
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)
DE	ScFv 6H8 protein (Fragment).	
GN	Name=ScFv 6H8;	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxId=10090;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=Balb/C;	
RC	MEDLINE=22853226; PubMed=12860977; DOI=10.1074/jbc.M306877200;	
RX	Peter J.C., Eftekhar P., Billiald P., Wallukat G., Hoebeke J.;	
RA	"scFv single chain antibody variable fragment as inverse agonist for	
RT	the beta-2 adrenergic receptor.";	
RU	J. Biol. Chem. 278:36740-36747 (2003).	
DR	EMBL; AJ574851; CAE00495.1; -.	
DR	HSSP; P01751; 1A6W.	
DR	InterPro; IPR007110; Ig_1like.	
DR	InterPro; IPR003596; Ig_V.	
DR	SMART; SMO0406; IGV; 2.	
DR	PROSITE; PS00835; IG_LIKE; 2.	
FT	NON TER 1	
SQ	SEQUENCE 243 AA; 25976 MW; BEFF642D2DC4F76 CRC64;	

Query Match		
Best Local Similarity	45.6%; Score 593; DB 2; Length 243;	
Matches 125; Conservative 33; Mismatches 77; Indels 10; Gaps 4;		
QY	1 QVQLVESGGGLVQPGGSLRLSCAASGTFPRSYAMSWRQAPGKLELVNSAISGRGDTTY 60	
DB	1 QVQLQSGSSESLVRPGASVKLSCKASGYFTFTYWMHWKORHGOLEWIGNIPGSGITNY 60	
QY	61 ADVSKGRTTISRDKSKNTLYIQNMSTLAEDPAVYCAKMTSNAPAFYWGQGLVTYSSG 120	
DB	61 DEKENKIKITLVDTSSSTAYMHLSTLASEDSAVYCAR---GGRGLDVGAGITLVSSG 117	
QY	121 GGGSGGGSGGGSGGQSVLTQ-PPSSVSGAPGQRTVISCTGSSSNIGAGYGVHWYQQLPGTA 179	
DB	118 GGGSGGGSGGGSGGSDIQMTGSSSFVSLDGRVITTCASBDIYNR---LAWYQKRGNA 174	
QY	180 PKLLIYGNTPSGVPPDRFSGFGKGTASLAITGLQADEADYICQPYDSLGSWVGGG 239	
DB	175 PRLIISGATSLIETGVPSPRFSGSGGKDYTLSTLSLTQTEDVAITYCCQGYWSTRT---FGCG 231	
QY	240 TKLTIV 244	
DB	232 TKLEI 236	

RESULT 7		
ID	Q92IA6	PRELIMINARY; PRT; 241 AA.
AC	Q92IA6	01-DEC-2001 (TREMBlrel. 19, Created)
DT	01-DEC-2001	(TREMBlrel. 19, Last sequence update)
DT	01-MAR-2004	(TREMBlrel. 26, Last annotation update)
DE	Anti-CEA 79 single chain Fv (Fragment).	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TaxId=10090;	

RN [1]
 SEQUENCE FROM N.A.
 RX MEDLINE=98170165; PubMed=9509426;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 YI K.S., Suh P.G., Ryu S.H., Chung H.K.;
 RT "Cloning and characterization of cDNA encoding VH and VL of a
 monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
 generation of a single-chain Fv molecule (scFv).";
 RL Mol. Cells 7:816-819(1997).
 DR EMBL; U88067; AAB48044.1; -.
 DR PIR; S19965; S19965.
 DR PIR; S19967; S19967.
 DR PIR; S19968; S19968.
 DR PIR; S26325; S26325.
 DR HSSP; P01607; 1BMW.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON_TER
 FT NON_TER 1
 SQ SEQUENCE 241 AA; 26086 MW; 0276887248E9C771 CRC64;

Query Match 45.5%; Score 592; DB 2; Length 241;
 Best Local Similarity 50.8%; Pred. No. 7e-34;
 Matches 128; Conservative 31; Mismatches 67; Indels 26; Gaps 8;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSATISGRDNTY- 59
 1 QVQLQSGDELKPKPSTVSKCAAGSYFTDYGMNWKQAPGKLEWGMV-----NTYT 55
 DB 60 ----YADSVKGRFTISRDNSKNTLYIQMNSLRPEDTVYVYCAKMTSNAPFDYWGQGLTV 115
 56 GEPYVADDFKGRPAFLETSASVAVYQINNLKNEEDVATYFCARDILRR-FDYWGQGLTV 114
 QY 116 TVSSGGGSGGSGGSGGSGGSGQSVLTQ-PPSVSGAPGQRTVITSGSSSNIGAGYGVHWYQ 174
 115 TVSSGGGSGGSGGSGGSGGSDILTQSPSLSSASLGKVTITTCASQD---INKYIANYQH 171
 DB 175 LFGTAPK---LIYGNTPRSGVDPDRFSGFKSGTISASLAIITGLQAEDEADYVYCOFYDSS 230
 172 KKGKGRSASHTLHY-----IQGIPSRFSGSGGRDYSPSISNLEPEDVATYCYCLHYDNL 227
 QY 231 LSGWVGSGTKL 242
 DB 228 ---HTFGGSGTKL 236

RESULT 8

065ZL2 PRELIMINARY; PRT; 487 AA.

AC 065ZL2;
 DT 25-OCT-2004 (TREMBlrel. 28, Created)
 DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
 DE FV/M4.
 GN Name=M4-IFN-<tau>;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96272580; PubMed=8668499;
 RA Qi Y., Xiang J.;
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
 antibody secreted from myeloma cells";
 RL Hum. Antibodies Hybridomas 6:161-166(1995).
 DR EMBL; S82493; AAB7424.2; -.
 DR InterPro; IPR003599; I9.
 DR InterPro; IPR007110; I9_1like.
 DR InterPro; IPR003597; I9_c1.
 DR InterPro; IPR003598; I9_c2.
 DR InterPro; IPR003006; I9_MHC.
 DR InterPro; IPR003596; I9_V.

DR Pfam; PF07654; Cl-set; 2.
 DR Pfam; PF00047; I9; 4.
 DR SMART; SM00409; I9; 3.
 DR SMART; SM00407; IGC1; 2.
 DR SMART; SM00408; IGC2; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PSS0835; IG_LIKE; 4.
 DR PROSITE; PSS0290; IG_MHC; UNKNOWN 1.
 SQ SEQUENCE 487 AA; 53578 MW; C7BAB69F3055504 CRC64;

Query Match 45.2%; Score 587; DB 2; Length 487;
 Best Local Similarity 48.0%; Pred. No. 3.3e-33;
 Matches 119; Conservative 42; Mismatches 69; Indels 18; Gaps 6;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSWVRQAPGKLEWVSATISGRDNTY 60
 20 QVQLQSDAEIVKPGASVYKISCAAGSYFTDHAHMAKQKPGLEWIGVISPNDIKY 79
 DB 61 ADSVYKGRFTISRDNSKNTLYIQMNSLRPEDTVYVYCAKMTSNAPFDYWGQGLTVVSSG 120
 80 NEKFKKATLTITADKSSSTAVYQINLSLSEDSAVYFCKRS-----YGHWGQGLTITL-GSG 133
 QY 121 GGGSGGSGGSGGSGGSGQSVLTQ-PPSVSGAPGQRTVITSGSS--SNIGAGYGVHWYQOLP 176
 134 GGGSGGSGGSGGSGGSGRIQMTQSPASLSVSGELVITTCRASENITSNLA-----WYQKQ 187
 QY 177 GAPKLLIYGNTPRSGVDPDRFSGFKSGTISASLAIITGLQAEDEADYVYCOFYDSSLSGWV 236
 188 GKSPQLVYAAITNLADGVPSRFRSGSGSGTQVSLKINSIQSEDFGSGYQGHFNG--TPYRF 245
 DB 237 GGGTKLTV 244
 DB 246 GGGTRLEI 253

RESULT 9

06GMX4 PRELIMINARY; PRT; 236 AA.

AC 06GMX4;
 DT 05-JUL-2004 (TREMBlrel. 27, Created)
 DT 05-JUL-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA TISSUE= spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altchul S.F., Zeeberg B., Buettow K.H., Scheffer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Wax S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.W., Hong L.,
 RA Stappleton M., Soares M.B., Bonaldo M.F., Cabaavanti T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueidi T.B., Toshiyuki S., Carninci P., Mullaby S.J.,
 RA Raha S.S., Lounellano N.A., Peters G.J., Abramson R.D., Mullaly P.H.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.

RC TISSUE=Spleen;
 RA Strauberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC073769; AAH73769.1; -
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PR07654; Cl-setc; 1.
 DR Pfam; PR00047; Ig; 2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00407; Igcl; 1.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 2.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1.
 DR Hypothetical protein.
 KW SEQUENCE 236 AA; 24809 MW; BA0AF04192364A5 CRC64;

Query Match 42.5%; Score 553; DB 2; Length 236;
 Best Local Similarity 91.4%; Pred. No. 3.7e-31;
 Matches 106; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 131 GGGSGSVLTQPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQQLPGTAPKLLIYGNTR 190
 DB 16 GSWAGSVLTQPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQQLPGTAPKLLIYGNTR 75
 QY 191 PGGVPDRFSGKSGTSASLAITGLQAEDEADYCCQYDSSLSGWSVGGGKTLTVLG 246
 DB 76 PGGVPDRFSGKSGTSASLAITGLQAEDEADYCCQYDSSLSGWSVGGGKTLTVLG 131

RESULT 10

Q96BB9 PRELIMINARY; PRT; 597 AA.

AC Q96BB9; PRELIMINARY; PRT; 597 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zieberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stadelton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usslin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loughellano N.A., Peters G.J., Abramson J.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Shaden A., Rodriguez S., Sanchez A.,
 RA Blakeley R.W., Medan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schmech A., Schein U.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strauberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL, BC015760; AAH15760.1; -
 DR PIR; S05271; S05271.
 DR PIR; S24260; S24260.
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR007110; Ig-like.
 DR InterPro; IPR003597; Ig_c1.
 DR InterPro; IPR003006; Ig_MHC.
 DR InterPro; IPR003596; Ig_v.
 DR Pfam; PR07654; Cl-setc; 4.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 DR SEQUENCE 597 AA; 65039 MW; 4FCA3AD8CE263D9 CRC64;

Query Match 41.2%; Score 535; DB 2; Length 597;
 Best Local Similarity 52.6%; Pred. No. 1.8e-29;
 Matches 122; Conservative 19; Mismatches 55; Indels 36; Gaps 5;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPRSYAMSVWROAPGKLEWVAISGRGNTYY 60
 DB 20 EQVLESGLVQPGGSLRLSCAASGFTPSYAMSVWROAPGKLEWVAISGSGSTYY 79
 QY 61 ADSVKGRFTISDNSENKTYLYLQNSLRADDTAVYICAK-----MTSNAFADPYGQGL 114
 DB 80 ADSVKGRFTISDNSENKTYLYLQNSLRADDTAVYICAKDPGYSAGNTREDYWGQGL 139
 QY 115 VTVSSGGSGSGSGSGSGSVLTQPSVSGAPGQRTVTSCTGSSSNIGAGYVHWYQ 173
 DB 140 VTVSSGS-----ASAPTLFPLVSGENSPDSTSSVAVGLAOD 176
 QY 174 QLPGTAPKLLIYGNTRPS---GVDPDRFSGKSGTSASLAITG---LQAEDE 219
 DB 177 FLDPDITFSWKTKKNSDISSTRGFPVSLGKRYATSGVTLPSKDVQGTDE 228

RESULT 11

Q925S1 PRELIMINARY; PRT; 218 AA.

AC Q925S1; PRELIMINARY; PRT; 218 AA.
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, last annotation update)
 DE MRPS (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RX PubMed=11819679;
 RA Cui D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
 RA Su C.;
 RT "Mechanism of exogenous nucleic acids and their precursors improving
 the repair of intestinal epithelium after irradiation in mice.";
 RL World J. Gastroenterol. 6:709-717(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c;
 RA Cui D., Zeng G., Yan X., Li X., Su C.;
 RT "Cloning of mouse genes related to repairing of intestinal epithelium
 of the irradiated mice by treatment with the intestinal RNA of mice of
 the same strain.";
 RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
 DR EMBL; AF240168; AAK43733.1; -
 DR HSSP; P01665; IQNZ.
 DR SMART; SM00406; IGV; 1.
 DR PROSITE; PS50835; IG_LIKE; 1.
 DR NON TER 218
 SO SEQUENCE 218 AA; 23013 MW; 527B4FA8F7982817 CRC64;

Query Match 40.6%; Score 527.5; DB 2; Length 218;
 Best Local Similarity 51.4%; Pred. No. 2.1e-29;

Matches 110; Conservative 32; Mismatches 67; Indels 5; Gaps 4;

QY 1 OYVLSGGGGLVQPGSLRLSCAAGFTRSYAMSVNRQAPKGLFWASIGRGNTY 60
 Db 3 QYVLSGGGGLVQPGSLRLSCAAGFTRSYAMSVNRQAPKGLFWASIGRGNTY 62
 QY 61 AYSVKGFTISRDNKNTLYLQNNSLRADTAVYVCARKNTSNAFADYWGOGTLVTVSSG 120
 Db 63 ABEFKRFAFSLSTASTAYLQSNKNEDTATYFCMRWDYDG-GFAYWGOGTLVTVSSG 121
 QY 121 GGGSGGGSGGGSGGSGVLTQ-PPSVSGAPGQRTVISTCTSSG--NTGAGYGVHWYQQLPG 177
 Db 122 GGGSGGGSGGGSGGSDVLTQSPASLAVSLGQRTATISCRASESYDNIGISF-MNMFQOKPG 180
 QY 178 TAPKLLIYGNTPRPSGVDRFSGFSGKSTGASLAI 211
 Db 181 QPKLLIYASKGGSGVPAGLASSGSDPRLNT 214

RESULT 12
 O6GMX3 PRELIMINARY; PRT; 236 AA.

AC O6GMX3, 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RX [1] TISSUE=Brain;
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Colling F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Strausberg R.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073770; AAH73770.1; -
 DR InterPro; IPR003597; IG_1
 DR InterPro; IPR007110; IG_1like
 DR InterPro; IPR003597; IG_1
 DR InterPro; IPR003006; IG_MHC
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF07654; Cl-set; 1
 DR Pfam; PF00047; Ig; 2
 DR SMART; SM00409; Ig; 2
 DR SMART; SM00407; IGC1; 1
 DR SMART; SM00406; IGV; 1
 DR PROSITE; PS00835; IG_LIKE; 2
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1

KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 24700 MW; BC0B394DF4F2DCB7 CRC64;

Query Match 40.2%; Score 523; DB 2; Length 236;
 Best Local Similarity 87.8%; Pred. No. 4.7e-29;
 Matches 101; Conservative 4; Mismatches 10; Indels 0; Gaps 0;

QY 131 GGGSGSVLTQPPSVSGAPGQRTVISTCTSSSNIGAGYGVHWYQQLPGTAPKLLIYGNTPR 190
 Db 16 GSMASQSVLTQPPSVSGAPGQRTVISTCTSSSNIGAGYGVHWYQQLPGTAPKLLIYGNTPR 75
 QY 191 PGGVDRFSGFSGKSTGASLAIQLQAEDEADYTCQFYDSSLSGWFPGGTTKTLTVL 245
 Db 76 PGGVDRFSGFSGKSTGASLAIQLQAEDEADYTCQFYDSSLSGWFPGGTTKTLTVL 130

RESULT 13
 O96E61 PRELIMINARY; PRT; 236 AA.

AC O96E61, 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NC NCB1_TaxID=9606;
 RX [1] TISSUE=Brain;
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Colling F.S., Wagner L., Shennan C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [12]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RA Strausberg R.;
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC012876; AAH12876.1; -
 DR PIR; S12440; S12440.
 DR HSSP; P01842; IAOK
 DR InterPro; IPR007110; IG_1like
 DR InterPro; IPR003597; IG_1
 DR InterPro; IPR003006; IG_MHC
 DR InterPro; IPR003596; IG_V
 DR Pfam; PF07654; Cl-set; 1
 DR SMART; SM00406; IGV; 1
 DR SMART; SM00407; IGC1; 1
 DR PROSITE; PS00835; IG_LIKE; 2
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_1
 KW Hypothetical protein.
 SQ SEQUENCE 236 AA; 24712 MW; 7EC9FB3622FED957 CRC64;

Query Match 39.8%; Score 518; DB 2; Length 236;
 Best Local Similarity 85.3%; Pred. No. 1.1e-28;

Matches 99; Conservative 4; Mismatches 13; Indels 0; Gaps 0;

QY 131 GGGSGGVLTPSPVSGAPGQRTVISTGSSSSNIGAGYGVHWYQOLPQTAPKLIYNTNR 190

DB 16 GSWAGSVLAPSPVSGAPGQRTVISTGSSSSNIGAGYGVHWYQOLPQTAPKLIYNTNR 75

QY 191 PGVPRPFGSGTSGTASLAITGLQAEDEADYTCQYDSSLGSMVGGGKTLTVLG 246

DB 76 PGVPRPFGSGTSGTASLAITGLQAEDEADYTCQYDSSLGSMVGGGKTLTVLG 131

RESULT 14

Q8WUK1 PRELIMINARY; PRT; 613 AA.

AC Q8WUK1; 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

OS IGHM protein. (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

NCBI_Taxid=9606;

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells; MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schler G.D.,

Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh F.,

Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Ueda T.B., Tohyuki S., Carninci P., Pearce C.,

Rabe S.S., Lonnellano N.A., Peters G.J., Abramson R.D., Millar S.J.,

Boeck S.A., McEwan P.J., McKernan K.J., Malek J.A., Guntur P.H.,

Richard S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Vallalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

Whiting M., Madan A.C., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

Krzywinski M.I., Skalski U., Smalins D.E., Scherch A., Schein J.E.,

Jones S.J., Maier M.A.,

"Generation and initial analysis of more than 15,000 full-length human

and mouse cDNA sequences."

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RP SEQUENCE FROM N.A.

RC TISSUE=Primary B-Cells; Straussberg R.;

RA Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC020240.1; RAH20240.1; -.

DR PIR; F36005; F36005.

DR PIR; G36005; F36005.

DR PIR; PH1642; PH1642.

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: April 19, 2005, 16:23:17 ; Search time 120.008 Seconds
(without alignments)
779.913 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267

Sequence: 1 QVQLVSGGGLVQPGGSLRLT.....QQYNYSYPLSFGGTYKVEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

A_Geneseq_16Dec04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1267	100.0	242	3	AAy58236 Internal
2	1084.5	85.6	239	7	ADG30447 Human GMB
3	1069	84.4	231	8	ADN06993 Human ERG
4	1065.5	84.1	233	4	AAg65715 Antino aci
5	1060.5	83.7	247	5	ABP45912 Human Bly
6	1060.5	83.5	247	5	ADG96739 Single ch
7	1058.5	83.5	239	5	ABP45911 Human Bly
8	1058.5	83.5	239	5	ADG96738 Single ch
9	1057.5	83.5	245	8	AAy06717 Antibody
10	1057.5	83.5	245	8	AD039736 Human c-m
11	1051.5	83.0	243	8	AD158047 Reg IV-ep
12	1050.5	82.9	239	5	ABP45871 Human Bly
13	1050.5	82.9	239	5	ADG96698 Single ch
14	1050	82.9	248	5	ABP45410 Human Bly
15	1050	82.9	248	5	ADG96237 Single ch
16	1048	82.7	240	4	AAAB6038 Human TF
17	1047	82.6	240	4	AAy02472 A single
18	1047	82.6	240	6	ABP95997 Human ser
19	1047	82.6	240	8	ADL92369 Human pha
20	1047	82.6	240	8	ADQ77165 HSA Heavy
21	1046	82.6	242	8	ADQ75289 Immunoglo
22	1046	82.6	250	8	ADQ40407 Single ch
23	1044.5	82.4	244	8	ADQ75290 Immunoglo
24	1044	82.4	240	7	ADG30465 Human GMB
25	1043.5	82.4	243	5	ABP45924 Human Bly

26	1043.5	82.4	243	7	ADG96751 Single ch
27	1041	82.2	240	4	AAAB6007 Human MUC
28	1041	82.2	249	8	ADQ40411 Single ch
29	1041	82.2	250	8	ADQ40410 Single ch
30	1040.5	82.1	245	2	AAy06714 Antibody
31	1040.5	82.1	245	8	AD039733 Human c-m
32	1040.5	82.1	251	5	ABP45299 Human Bly
33	1040.5	82.1	251	7	ADG96126 Single ch
34	1040	82.1	241	2	AAW24063 Human MSX
35	1040	82.1	241	7	ADCO8951 Human MSX
36	1039	82.0	291	8	ADN06992 Human ERG
37	1037	81.8	240	4	AAAB6039 Human TF
38	1034	81.6	240	4	AAAB6040 Human TF
39	1033.5	81.6	243	5	ABP45934 Human Bly
40	1033.5	81.6	243	7	ADG96761 Single ch
41	1032	81.5	239	5	AAU90905 Insulin/I
42	1032	81.5	240	4	AAAB6020 Human MUC
43	1031	81.4	244	5	ABP44071 Human Bly
44	1031	81.4	244	7	ADG94898 Single ch
45	1030	81.3	240	4	AAAB5999 Human MUC

ALIGNMENTS

RESULT 1	
ID	AAy58236
AC	AAy58236 standard; protein; 242 AA.
DT	27-MAR-2000 (first entry)
DE	Internalising anti-c-erbB-2 receptor antibody scFv C1.
KW	Antibody; c-erbB-2 receptor; marker; cancer; drug targeting;
OS	HER/neu oncogene; tumour-specific; internalisation; non-immunogenic.
XX	Synthetic.
XX	Homo sapiens.
XX	Location/Qualifiers
FT	Key
FT	Region
FT	/note="Heavy chain variable region (VH) complementarity determining region 1 (CDR1)"
FT	/note="Encoded by GTM"
FT	Region
FT	/note="VH-CDR2"
FT	/note="VH-CDR3"
FT	Region
FT	/note="Light chain variable region (VL) complementarity determining region 1 (CDR1)"
FT	/note="VL-CDR2"
FT	/note="VL-CDR3"
FT	Region
XX	WO9955367-A1.
XX	PD
XX	04-NOV-1999.
XX	PF
XX	23-APR-1999; 99WO-US007395.
XX	XX
XX	24-APR-1998; 98US-0082953P.
XX	PR
XX	12-FEB-1999; 99US-00250056.
XX	PA
XX	(REGC) UNIV CALIFORNIA.
XX	ADQ75290 Immunoglo
XX	ADQ75290 Immunoglo
XX	ADQ30465 Human GMB
XX	ABP45924 Human Bly
XX	WPI; 2000-072168/06.

DR N-PSDB; AA255615.

XX Novel internalizing antibodies used to treat cancer cells.

XX Claim 3; Page 82; 85pp; English.

XX This sequence represents an internalising humanised antibody, scFv C1, which specifically binds to the extracellular domain of the c-erbB-2 receptor, the protein product of the HER/neu oncogene. The scFv C1 antibody binds to the epitope of the c-erbB-2 receptor that is bound by C1 antibodies. On binding the c-erbB-2 receptor, the antibody is transported into the cell. The c-erbB-2 receptor is a marker protein which is overexpressed by 30-50% of breast carcinomas and other adenocarcinomas, and thus provides a useful cell surface marker for specifically targeting tumour cells. The antibodies of the invention are used as tumour-targeting molecules for diagnosis and treatment. The antibodies can be attached to effector molecules. The effector molecules may include cytotoxins such as ricin, abrin or Pseudomonas exotoxin, radionuclides, ligands such as growth factors, therapeutic agents such as vinblastine, vindesine or melphalan; ribozymes; or antisense molecules. The antibodies may also be used for in vivo or in vitro detection and/or quantitation of the c-erb-2 receptor and thus diagnosis and/or localisation of cancers characterised by expression of c-erb-2. Although antibodies have previously been used to target tumour cells, their success has been limited. The utility of prior art antibodies has been hampered by the paucity of tumour specific antibodies, antibody immunogenicity, low binding affinity, and poor tumour penetration. Immunogenicity could be avoided and toxicity reduced if high affinity tumour specific human antibodies were available. However, the production of human monoclonal antibodies using conventional hybridoma technology has proven difficult. Also, most of the antibodies produced react with antigens that are also common to non-malignant cells, which makes them unsuitable for use as tumour-targeting molecules. The antibodies of the invention overcome these difficulties, as they are targeted to a tumour-specific antigen, and avoid the problem of immunogenicity as they are human in origin.

XX Sequence 242 AA;

Query Match 100.0%; Score 1267; DB 3; Length 242;
Best Local Similarity 100.0%; Pred. No. 5.7e-82;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTSSYAMGVNRPQKGLIEWSSISGSSRYIY 60
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTSSYAMGVNRPQKGLIEWSSISGSSRYIY 60
QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIVYCAKMDAGSYNPNFGQGLTVVSSG 120
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIVYCAKMDAGSYNPNFGQGLTVVSSG 120
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180
DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180
QY 181 LIYAASLTQSGVPSRFSGSGSDTFTLTSSIQPEDFATYYCOQNSYPLSLFGGKTKVEI 240
DB 181 LIYAASLTQSGVPSRFSGSGSDTFTLTSSIQPEDFATYYCOQNSYPLSLFGGKTKVEI 240
QY 241 KR 242
DB 241 KR 242

RESULT 2

ADG30447 standard; protein; 239 AA.

AC ADG30447;

DT 26-FEB-2004 (first entry)

DE Human GMB655 scFv protein.

XX GMAD; VH; CDR; complementarity determining region; VL; scFv;
KW single chain antibody; antidiabetic; type II diabetes; human; GMB655.
XX Homo sapiens.

XX WO2003085093-A2.

XX 16-OCT-2003.

XX 28-MAR-2003; 2003WO-US009625.

XX 01-APR-2002; 2002US-036813P.

XX (HUMA-) HUMAN GENOME SCI INC.

XX Baker KP, Albert VR, Chowdhury P;

XX WPI, 2003-804305/75.

XX N-PSDB; ADG30544.

XX New antibody that specifically binds to GMAD polypeptide, useful for diagnosing, monitoring, treating, preventing or ameliorating type II diabetes.

XX Claim 2; SEQ ID NO 80; 410pp; English.

XX The invention relates to a novel antibody that specifically binds to a GMAD polypeptide comprising a first amino acid sequence that is at least 95% identical to a second amino acid sequence of a VH CDR (single chain antibody molecule). The antibody of the invention demonstrates antidiabetic activity and may be useful for diagnosing, monitoring, treating, preventing or ameliorating type II diabetes. The current sequence is that of the human scFv protein of the invention.

XX Sequence 239 AA;

Query Match 85.6%; Score 1084.5; DB 7; Length 239;
Best Local Similarity 85.1%; Pred. No. 4.7e-69;
Matches 206; Conservative 16; Mismatches 17; Indels 3; Gaps 1;

QY 1 QVQLVSGGGLVQPGSLRLSCAASGFTSSYAMGVNRPQKGLIEWSSISGSSRYIY 60
DB 1 EVQLVESGGGLVQPGSLRLSCAASGFTSSYAMGVNRPQKGLIEWSSISGSSRYIY 60
QY 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIVYCAKMDAGSYNPNFGQGLTVVSSG 120
DB 61 ADSVKGRTISRDNKNTLYLQWNSLRADTAIVYCAKMDAGSYNPNFGQGLTVVSSG 117
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 180
DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPGKAPKL 177
QY 181 LIYAASLTQSGVPSRFSGSGSDTFTLTSSIQPEDFATYYCOQNSYPLSLFGGKTKVEI 240
DB 181 LIYAASLTQSGVPSRFSGSGSDTFTLTSSIQPEDFATYYCOQNSYPLSLFGGKTKVEI 237
QY 241 KR 242
DB 238 KR 239

RESULT 3

ADN06993 standard; protein; 291 AA.

AC ADN06993;

DT 01-JUL-2004 (first entry)

DE Human ERGR bs-scFv antibody protein, EGFR.B8.

KW Bispecific single chain; bs-scfv; cancer;
 KW epidermal growth factor receptor; EGFR; therapy; antibody; human.
 OS Homo sapiens.
 XX US2004071696-A1.
 XX PD 15-APR-2004.
 XX PF 04-APR-2003; 2003US-00406830.
 XX PR 05-APR-2002; 2002US-0370276P.
 XX PA (REGC) UNIV CALIFORNIA.
 XX PA (FOXC-) FOX CHASE CANCER CENT.
 XX PI Adams GP, Horak EM, Weiner LM, Marks JD;
 XX WPI; 2004-328525/30.
 XX DR WPI; 2004-328525/30.
 XX PT Novel bispecific antibody comprising first and second antibody joined to
 PT each other and having binding specificity to different epitopes of
 PT Epidermal Growth Factor Receptor protein, useful for treating cancer.
 XX PS Claim 14; SEQ ID NO 10; 57pp; English.
 XX CC The present invention provides bispecific single chain (bs-scfv) antibody
 CC molecules which may be used to treat various forms of cancer associated
 CC with the overexpression of the epidermal growth factor receptor (EGFR)
 CC family. The invention is useful for specifically delivering an effector
 CC molecule to a cell bearing a receptor from EGFR protein family chosen
 CC from EGFR, HER2/neu, HER3 and HER4. The invention is useful in the
 CC treatment of cancer. The present sequence is human EGFR bs-scfv antibody
 CC protein.
 XX SQ Sequence 291 AA;
 Query Match 84.4%; Score 1069; DB 8; Length 291;
 Best Local Similarity 84.1%; Pred. No. 7, 2e-68;
 Matches 207; Conservative 13; Mismatches 22; Indels 4; Gaps 1;
 QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTPSVAMGVRAQPGKLEWVSISGSSRYIYY 60
 DB 23 QVQLVSGGGLVPGGSLRLSCAASGFTPSVAMGVRAQPGKLEWVSISGSSRYIYY 82
 QY 61 ADSVKRFTISRDNKNTLYLQWNSLRADPTALYYCARREGYSNNMNYFDLGRGTLVT 116
 DB 83 ADSVKRFTISRDNKNTLYLQWNSLRADPTALYYCARREGYSNNMNYFDLGRGTLVT 142
 QY 117 VSSGGGSGGSGGSGGSETTLTQSPPLSAFVGDRIITTCRASPGIRNYLAWYQKPKG 176
 DB 143 VSSGGGSGGSGGSGGSEIVLTQSPSLASAVGDRVITTCRASQSSISLAWYQKPKG 202
 QY 177 APRLLIYAASLTQSGVPSRPSGSGTDTFTLTITSSIQPEDFATYYCOQYNSYPLSGGCT 236
 DB 203 APRLLIYAASLTQSGVPSRPSGSGTDTFTLTITSSIQPEDFATYYCOQYNSYPLSGGCT 262
 QY 237 KVEIKR 242
 DB 263 KLEIKR 268
 RESULT 4
 ID AAG65715 standard; protein; 293 AA.
 XX AAG65715;
 XX AC AAG65715;
 XX DT 07-JAN-2002 (first entry)
 XX XX Amino acid sequence of secreted form of scFv 4A.
 XX DE Polymeric immunoglobulin receptor; pIgR; ligand; therapeutic;
 XX KW

KW carcinoma diagnosis; veterinary; scFv 4A.
 XX Synthetic.
 OS Key
 XX Peptide
 XX Location/Qualifiers
 FT 1..22
 FT /note= "peb leader"
 FT 23..27
 FT /note= "FLAG epitope"
 FT 28..58
 FT /note= "Heavy chain framework 1"
 FT 59..62
 FT /note= "CDR1"
 FT 63..76
 FT /note= "Heavy chain framework 2"
 FT 77..93
 FT /note= "CDR2"
 FT 94..125
 FT /note= "Heavy chain framework 3"
 FT 126..139
 FT /note= "CDR3"
 FT 140..147
 FT /note= "Heavy chain framework 4"
 FT 148..162
 FT /note= "linker"
 FT 163..185
 FT /note= "light chain framework 1"
 FT 186..196
 FT /note= "CDR1"
 FT 197..211
 FT /note= "light chain framework 2"
 FT 212..218
 FT /note= "CDR2"
 FT 219..250
 FT /note= "light chain framework 3"
 FT 251..259
 FT /note= "CDR3"
 FT 260..270
 FT /note= "light chain framework 4"
 FT 274..283
 FT /note= "myc epitope tag"
 FT 288..293
 FT /note= "6 His tag"
 PN WO200172846-A2.
 XX 04-OCT-2001.
 XX 26-MAR-2001; 2001WO-US009699.
 XX 27-MAR-2000; 2000US-0192197P.
 XX 27-MAR-2000; 2000US-0192198P.
 XX (REGC) UNIV CALIFORNIA.
 XX Mostov KE, Chapin SJ, Richman-Eisenstat J;
 XX WPI; 2001-611619/70.
 XX New ligands binding to a specific region of a polymeric immunoglobulin
 XX receptor, useful for transporting therapeutic or diagnostic compositions
 XX into or across cells expressing pIgR e.g. in drug delivery.
 XX Disclosure; Fig 5; 102pp; English.
 XX The invention provides ligands that bind specifically to a region of an
 XX animal cell polymeric immunoglobulin receptor (pIgR). The pIgR cleaves to
 XX produce a stalk region remaining attached to the cell and a secretory
 XX component existing in the organ of interest in several forms. The ligands
 XX do not bind to the stalk or the most abundant form of the secretory
 XX component present in the organ under physiological conditions. The
 XX ligands are useful for transporting therapeutic or diagnostic
 XX compositions into or across cells expressing pIgR, useful to introduce or

CC transport ligands such as antibodies and/or to deliver biologically
 CC active components such as proteins, nucleic acids or detectable labels.
 CC They are used to deliver therapeutic compositions to mucosal surfaces
 CC such as the gastro-intestinal tract, respiratory system etc. in humans.
 CC They are also useful to label cells expressing pIgR, e.g. to distinguish
 CC epithelial cells from a mixed cell population in pathology studies or to
 CC aid in carcinoma diagnosis (since pIgR expression is reduced in
 CC carcinomas relative to normal epithelium). They can also be used to
 CC deliver veterinary compositions, especially in mammals such as farm,
 CC domestic or wild mammals or birds e.g. birds reared for human
 CC consumption. The present sequence represents the amino acid sequence of
 CC secreted form of scFv 4A
 XX
 XX
 SQ Sequence 293 AA;

Query Match 84.1%; Score 1065.5; DB 4; Length 293;
 Best Local Similarity 84.8%; Pred. No. 1.3e-67;
 Matches 206; Conservative 12; Mismatches 24; Indels 1; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGVRAQPGKLEWVSISGSSRIYY 60
 |||||
 DB 28 QVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMGVRAQPGKLEWVSISGSSRIYY 87
 |||||
 QY 61 AASVKRFTISRDNKNTLYLQNSLRADTAIVYCAK-MDASGSYFNWGQTLVTVSS 119
 |||||
 DB 88 ADSVKGRFTISRDNKNTLYLQNSLRADTAIVYCAKSFYVNSGYFQHMGGTTLTVSS 147
 |||||
 QY 120 GGGSGGGSGGGSGGSETTLTQSPFLAFVDRITTCRASPCIRNYLAWYQOKPKAKP 179
 |||||
 DB 148 GGGSGGGSGGGSGGSETTLTQSPFLAFVDRITTCRASPCIRNYLAWYQOKPKAKP 207
 |||||
 QY 180 LLIYAASLTQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSFGGTYE 239
 |||||
 DB 208 LLIYKASLSAGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSFGGTYE 267
 |||||
 QY 240 IKR 242
 |||||
 DB 268 IKR 270

RESULT 5

ABP45912
 ID ABP45912 standard; protein; 247 AA.

AC ABP45912;

DT 19-AUG-2002 (first entry)

DE Human BlyS binding scFv SEQ ID 1923.

XX BlyS; B lymphocyte stimulator; TNF superfamily; human; cytosolic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.

XX Homo sapiens.

XX MO200202641-A1.

PD 10-JAN-2002.

PF 15-JUN-2001; 2001WO-US019110.

XX 16-JUN-2000; 2000US-0212210P.

PR 17-OCT-2000; 2000US-0240816P.

PR 16-MAR-2001; 2001US-0276248P.

PR 21-MAR-2001; 2001US-0277379P.

XX 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D,
 PI WPI; 2002-114799/15.
 DR

PT Antibodies against B Lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

XX Claim 1; Page 2695-2696; 3148pp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (BlyS) polypeptides. BlyS is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of BlyS. The antibodies bind to BlyS
 CC and so may be used to detect and quantitate the presence of BlyS in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of BlyS. They may also be
 CC administered to treat diseases associated with aberrant BlyS expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 XX
 XX
 SQ Sequence 247 AA;

Query Match 83.7%; Score 1060.5; DB 5; Length 247;
 Best Local Similarity 82.2%; Pred. No. 2.4e-67;
 Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGVRAQPGKLEWVSISGSSRIYY 60
 |||||
 DB 1 EVQLVQSGGGLVQPGGSLRLSCAASGFTFSYAMGVRAQPGKLEWVSISGSSRIYY 60
 |||||
 QY 61 ADSVKRFTISRDNKNTLYLQNSLRADTAIVYCAKMDA--SGS--YFNWGQTLV 115
 |||||
 DB 61 ADSVKRFTISRDNKNTLYLQNSLRADTAIVYCAKMDA--SGS--YFNWGQTLV 120
 |||||
 QY 116 TVSSGGGSGGGSGGSETTLTQSPFLAFVDRITTCRASPCIRNYLAWYQOKPKG 175
 |||||
 DB 121 TVSSGGGSGGGSGGSETTLTQSPFLAFVDRITTCRASPCIRNYLAWYQOKPKG 180
 |||||
 QY 176 KAPKLLIYAASLTQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSFGG 235
 |||||
 DB 181 KAPKLLIYAASLTQSGVPSRFSGSGGTDTFTLTISLQPEDPATYVCCQYNSYPLSFGG 240
 |||||
 QY 236 TVEIKR 242
 |||||
 DB 241 TKLKIKR 247
 |||||

RESULT 6

ADG96739
 ID ADG96739 standard; protein; 247 AA.

AC ADG96739;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds BlyS SeqID 1923.

XX antibody; B lymphocyte stimulator; BlyS; tumour necrosis factor;
 KW B cell proliferation; differentiation; scFv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukemia;
 KW carcinoma; lymphoma; antirheumatic; antirheumatic; neuroprotective;
 KW antiinflammatory; antiaesthetic; antiasthmatic; cytostatic.

XX Unidentified.

PN WO2003055979-A2.
XX
XX 10-JUL-2003.
XX
XX 14-NOV-2002; 2002WO-US036496.
XX
XX 16-NOV-2001; 2001US-0331469P.
XX PR 19-DEC-2001; 2001US-0340817P.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;
XX WPI; 2003-505530/47.
XX
XX Novel antibody that immunospecifically binds to a B lymphocyte stimulator
XX (Blys), useful for detecting and treating diseases or disorders e.g.
XX rheumatoid arthritis, asthma and leukemia.

XX Example 1; SEQ ID NO 1923; 394bp; English.

CC This invention relates to novel antibodies that immunospecifically bind
CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
CC chromosome 13q34 and encodes a protein that is a member of the tumour
CC necrosis factor superfamily and induces both in vivo and in vitro B cell
CC proliferation and differentiation. Specifically, it refers to single
CC chain antibody molecules (scFvs) derived, preferably, from the variable
CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
CC fragment thereof, of either human, murine, rat or monkey Blys. The
CC present invention refers to the use of such antibodies in various methods
CC for the detection, diagnosis and prognosis of diseases related to the
CC aberrant expression or inappropriate function of Blys or its receptor. As
CC such, these compositions are useful for identifying immune disorders
CC including myasthenia gravis and multiple sclerosis, inflammatory
CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
CC as AIDS and proliferative disorders including leukaemia, carcinoma and
CC lymphoma. Accordingly, they can be described as exhibiting various
CC activities such as antineoplastic, antitumour, neuroprotective,
CC antiinflammatory, antiasthmatic, antiallergic and cytostatic. This
CC polypeptide sequence is a single chain antibody that binds Blys of the
CC invention. NOTE: The sequence data for this patent did not form part of
CC the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published pct_sequences.

XX Sequence 247 AA;

Query Match 83.7%; Score 1060.5; DB 7; Length 247;
Best Local Similarity 82.2%; Pred. No. 2,4e-67;
Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPGKGLEWVSISGSSRIYY 60
DB 1 EVQLVSGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKGLEWVAISGSGSTYY 60
QY 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAKMDA---SGS--YFNWGGCTLV 115
DB 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAKAGNRSGLVYFDWGRRTWY 120
QY 116 TVSSGGGGGGGGGGGGSTFTLTQSPSFSLAVGDRITITTCASPGIRNYLAWYQKPG 175
DB 121 TVSSGGGGGGGGGGGGSTFTLTQSPSTLSASIGRVITTCASPGIRNYLAWYQKPG 180
QY 176 KAPKLLIVASTQSGVPSRFSGSGGTFTLTSSIQPEDPATYVYCOQVNSYPLSRGGG 235
DB 181 KAPKLLIVKASLSAAPSRSFGSGGTFTLTSSIQPEDPATYVYCOQVNSYPLSRGGG 240
QY 236 TKVEIKR 242
DB 241 TKVKIKR 247

RESULT 7
ABP45911

ID ABP45911 standard; protein; 239 AA.

XX AC ABP45911;

XX XX 19-AUG-2002 (first entry)

XX DE Human Blys binding scFv SEQ ID 1922.

XX Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
XX tumour necrosis factor; B cell proliferation; B cell differentiation;
XX immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
XX antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
XX systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
XX common variable immunodeficiency; acquired immunodeficiency syndrome.

XX OS Homo sapiens.

XX PN WO200202641-A1.

XX PD 10-JAN-2002.

XX PF 15-JUN-2001; 2001WO-US019110.

XX PR 16-JUN-2000; 2000US-0212210P.

XX PR 17-OCT-2000; 2000US-0240816P.

XX PR 16-MAR-2001; 2001US-0276248P.

XX PR 21-MAR-2001; 2001US-0277379P.

XX PR 25-MAY-2001; 2001US-0293499P.

XX PA (HUMA-) HUMAN GENOME SCI INC.

XX PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.

XX PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;

XX DR WPI; 2002-114799/15.

XX PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the

XX diagnosis and treatment of cancers and immune disorders.

XX PS Claim 1; Page 2694-2695; 3148bp; English.

CC This invention describes novel antibodies that immunospecifically bind to
CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
CC tumour necrosis factor (TNF) super family and induces B cell
CC proliferation and differentiation. The antibodies of the invention have
CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
CC antineoplastic and antiAIDS activity and can be used in vaccines to
CC inhibit the expression and activity of Blys. The antibodies bind to Blys
CC and so may be used to detect and quantitate the presence of Blys in
CC biological samples and may be used in this way to diagnose disease
CC associated with aberrant expression of Blys. They may also be
CC administered to treat diseases associated with aberrant Blys expression
CC and activity such as cancer, immune, and autoimmune disorders and
CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
CC the antibodies and fragments of the antibodies described in the method of
CC the invention

XX Sequence 239 AA;

Query Match 83.5%; Score 1058.5; DB 5; Length 239;
Best Local Similarity 83.5%; Pred. No. 3.3e-67;
Matches 202; Conservative 18; Mismatches 19; Indels 3; Gaps 1;

QY 1 QVQLVSGGGLVPGGSLRLSCAASGFTFSYAMGWROAPGKGLEWVSISGSSRIYY 60
DB 1 EVQLVETGGGLVPGGSLRLSCAASGFTFSYAMSWROAPGKGLEWVAISGSGSTYY 60
QY 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAKMDASGSYFNWGGCTLVYSSG 120
DB 61 ADSVKRFTISRDNKNTLYLQNSLRADDTAVYYCAK---GWRGVYDWGRGLTVYSSG 117

(TPO). They can stimulate proliferation, differentiation or growth of megakaryocytes. They may also be able to stimulate megakaryocytes to increase platelet production. They can be used for treating immunological or hematopoietic disorders, especially thrombocytopenia. Thrombocytopenia -associated bone marrow hypoplasia (e.g. aplastic anemia following chemotherapy or bone marrow transplant) may be effectively treated with the antibody compounds as well as disorders such as disseminated intravascular coagulation (DIC), immune thrombocytopenia (HIV-induced and non HIV-induced), chronic idiopathic thrombocytopenia, congenital thrombocytopenia, thrombotic thrombocytopenia and myelodysplasia. They can also be used in e.g. myelotoxic chemotherapy for treatment of solid tumours or leukaemia, myeloablative chemotherapy for autologous or allogeneic bone marrow transplant, myelodysplasia, idiopathic aplastic anemia, congenital thrombocytopenia, and immune thrombocytopenia. The antibodies which bind to the MusK receptor can be used for improving neuromuscular function in a patient, e.g. in muscular dystrophy. The products can also be used for detection and diagnosis. The antibodies have a longer half-life than the natural ligand for the TPO-R. Sequences AA06713-Y06718 represent single chain Fv (scFv) fragments of various antibodies

Sequence 245 AA:

Query Match 83.5%; Score 1057.5; DB 2; Length 245;
Best Local Similarity 83.1%; Pred. No. 3.9e-67;
Matches 201; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVSSGGGLVOPGSGSLRLSCAASGFTPSYAMGVWROAPGKLEWVSSISGSSRYIYY 60
DB 3 QVQLVSSGGGLVOPGSGSLRLSCAASGFTPSYAMGVWROAPGKLEWVSSISGSSRYIYY 62
QY 61 ADSVKGRFTISRDNKNTLYLQNSSLRAEDTAVYYCAKMDASGSYENFMQGTLYTVSSG 120
DB 63 ADSVKGRFTISRDNKNTLYLQNSSLRAEDTAVYYCAR-DRGSTGMDVMGRGLTVTVSSG 121
QY 121 GGGSGGGSGGGSEETLTQSPFSLAFAVGDRTITTCRASPGIRNYLAWYQKRGAPKL 180
DB 122 GGGSGGGSGGGSDIQMTQSPSLASIGDRVITTCRASBGIVHWLAWYQKRGAPKL 181
QY 181 LIYAASLTQSGVPSRSGSGSDFTLTISLQPEPATYYCCQVNSYPLSPFGGRTKVEI 240
DB 182 LIYKASLASGAPSRSGSGSDFTLTISLQPDFAIYYCCQVNSYPLSPFGGRTKLEI 241
QY 241 KR 242
DB 242 KR 243

RESULT 10
ADO39736
ID ADO39736 standard; protein; 245 AA.

XX AC ADO39736;
XX DT 29-JUL-2004 (first entry)
XX DE Human c-mpl single chain agonist antibody fragment (scFv) protein, 12DS.
XX KW Variable heavy chain; VH; variable light chain; VL; c-mpl antibody; CDR; haemostatic; haematopoietic disorder; thrombocytopenia; gene therapy; antibody; agonist; human; single chain antibody fragment; scFv.
XX OS Homo sapiens.

XX FH Key Location/Qualifiers
FT Region 33..37
FT /note= "VH CDR1"
FT Region 52..73
FT /note= "VH CDR2"
FT Region 101..109
FT /note= "VH CDR3"
FT Region 159..169
FT /note= "VL CDR1"

FT Region 185..191
FT /note= "VL CDR2"
FT Misc-difference 208
FT /label= Unknown
FT /note= "Xaa may be any amino acid"
FT Region 224..232
FT /note= "VL CDR3"

PN US6737249-B1.

PD 18-MAY-2004.

XX 21-AUG-1998; 98US-00138091.

PR 22-AUG-1997; 97US-0056736P.

XX (GETH) GENENTECH INC.

PI Adams CW, Carter PJ, Fendly BM, Gurney AL;

DR WPI; 2004-387096/36.

PT New nucleic acid encoding human c-mpl agonist antibody comprising Ab1, Ab2, Ab3, Ab4, Ab5 or Ab6, useful in preparing a composition for treating hematopoietic disorders, e.g., thrombocytopenia.

PS Disclosure; SEQ ID NO 76; 58pp; English.

XX The present invention relates to human c-mpl antibodies comprising Ab1, Ab2, Ab3, Ab4, Ab5 and Ab6 each of which comprises a VH and VL chain comprising CDR amino acid sequences designated CDR1, CDR2 and CDR3 and their encoding nucleic acids. The invention acts as a haemostatic agent and is useful for treating haematopoietic disorders such as thrombocytopenia. The invention is also useful in gene therapy. The present sequence is human c-mpl single chain agonist antibody fragment (scFv) protein.

XX Sequence 245 AA;

Query Match 83.5%; Score 1057.5; DB 8; Length 245;
Best Local Similarity 83.1%; Pred. No. 3.9e-67;
Matches 201; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVSSGGGLVOPGSGSLRLSCAASGFTPSYAMGVWROAPGKLEWVSSISGSSRYIYY 60
DB 3 QVQLVSSGGGLVOPGSGSLRLSCAASGFTPSYAMGVWROAPGKLEWVSSISGSSRYIYY 62
QY 61 ADSVKGRFTISRDNKNTLYLQNSSLRAEDTAVYYCAKMDASGSYENFMQGTLYTVSSG 120
DB 63 ADSVKGRFTISRDNKNTLYLQNSSLRAEDTAVYYCAR-DRGSTGMDVMGRGLTVTVSSG 121
QY 121 GGGSGGGSGGGSEETLTQSPFSLAFAVGDRTITTCRASPGIRNYLAWYQKRGAPKL 180
DB 122 GGGSGGGSGGGSDIQMTQSPSLASIGDRVITTCRASBGIVHWLAWYQKRGAPKL 181
QY 181 LIYAASLTQSGVPSRSGSGSDFTLTISLQPEPATYYCCQVNSYPLSPFGGRTKVEI 240
DB 182 LIYKASLASGAPSRSGSGSDFTLTISLQPDFAIYYCCQVNSYPLSPFGGRTKLEI 241
QY 241 KR 242
DB 242 KR 243

RESULT 11

ADIS8047
ID ADIS8047 standard; protein; 243 AA.

XX ADIS8047;

XX 22-APR-2004 (first entry)

Reg IV-specific single chain antibody fragment (scFv) #6.

XX antibody; regeneration IV; Reg IV; single chain antibody fragment; scFv;
 KW inflammatory bowel disorder; ulcerative colitis; Crohn's disease;
 KW diabetes; non-insulin dependent diabetes; insulin dependent diabetes;
 KW cancer; human.
 XX
 OS Homo sapiens.
 XX
 XX WO2004003144-A2.
 XX
 PD 08-JAN-2004.
 XX
 XX 26-JUN-2003; 2003WO-US019908.
 XX
 XX 01-JUL-2002; 2002US-0392382P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA;
 XX
 DR WPI; 2004-071976/07.
 DR N-PSDB; AD158113.
 XX
 PT Novel antibody, useful for treating, preventing or ameliorating
 PT inflammatory bowel disorder, cancer of the gastrointestinal tract or
 XX diabetes (non-insulin dependent diabetes or insulin dependent diabetes).
 XX
 PS Claim 2; SEQ ID NO 6; 324bp; English.

CC The invention comprises an antibody that specifically binds a
 CC regeneration IV (Reg IV) protein. The invention specifically comprises
 CC the amino acid and coding sequences of single chain antibody fragments
 CC (scFV's) that bind Reg IV protein. The antibody of the invention is
 CC useful for treating, preventing and ameliorating: inflammatory bowel
 CC disorders (e.g. ulcerative colitis or Crohn's disease), diabetes (e.g.
 CC non-insulin dependent diabetes or insulin dependent diabetes), and cancer
 CC of the gastrointestinal tract. The antibody of the invention is also
 CC useful for detecting the expression of a Reg IV protein. The present
 CC amino acid sequence represents an scFv of the invention.

XX Sequence 243 AA;

Query Match 83.0%; Score 1051.5; DB 8; Length 243;
 Best Local Similarity 83.7%; Pred. No. 1e-66;
 Matches 205; Conservative 14; Mismatches 21; Indels 5; Gaps 2;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKGLEWVSISGSSRRYY 60
 DB 1 EVQLVQSGGGLVQPGKSLRLSCAASGFTSSVGMVRAQPGKGLEWAVISIDGSNKYY 60
 QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAKMDAGSY---FNFVQGGTLTV 117
 DB 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK---ASTYYVFWFDINGCGIMTV 118
 QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK---ASTYYVFWFDINGCGIMTV 118
 DB 118 SSGGGGGGGGGGGSETTLTQSPFSLAFAVGDRIITTCRASPGIRNYLAWYQKPKA 177
 DB 119 SSGGGGGGGGGGGSGSDIQMTQSPSFLASVDRVITTCRASQGINNYLAWYQKPKA 178
 QY 178 PKLLITAASTLQSGVSRPSSGSGGCGDPTLTITSLQPPFATYYCCQVNSYPLSPFGGK 237
 DB 179 PKLLITAASTLQSGVSRPSSGSGGTDPTLTITSLQPPFATYYCLQSDSDYPLTFGGGK 238
 QY 238 VEIKR 242
 DB 239 LEIKR 243

RESULT 12
 ABP45871
 XX ID ABP45871 standard; protein; 239 AA.
 AC ABP45871;
 XX

DT 19-AUG-2002 (first entry)
 XX
 DE Human Blys binding scFv SEQ ID 1882.
 XX
 KW Blys; B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KW tumour necrosis factor; B cell proliferation; B cell differentiation;
 KW immunosuppressive; immunostimulant; immunomodulatory; antirheumatic;
 KW antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KW systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KW common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 XX WO200202641-A1.
 XX
 XX 10-JAN-2002.
 XX
 PD 15-JUN-2001; 2001WO-US019110.
 XX
 XX 16-JUN-2000; 2000US-0212210P.
 XX
 XX 17-OCT-2000; 2000US-0240816P.
 XX
 XX 16-MAR-2001; 2001US-0276248P.
 XX
 XX 21-MAR-2001; 2001US-0277379P.
 XX
 XX 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CAMP-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 XX
 DR WPI; 2002-114799/15.

PT Antibodies against B lymphocyte Stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.

PS Claim 1; Page 2647-2648; 3148bp; English.

CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte Stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX Sequence 239 AA;

Query Match 82.9%; Score 1050.5; DB 5; Length 239;
 Best Local Similarity 81.8%; Pred. No. 1.2e-66;
 Matches 198; Conservative 23; Mismatches 18; Indels 3; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSVAMGVRAQPGKGLEWVSISGSSRRYY 60
 DB 1 QVQLVQSGGGLVQPGKSLRLSCAASGFTSSVGMVRAQPGKGLEWAVISIDGSNKYY 60
 QY 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK---FNFVQGGTLTVVSSG 120
 DB 61 ADSVKGKFTISRDNKNTLYLQWNSLRADTAIVYCAK---TGSDFVWGRGTLTVVSSG 117
 QY 121 GGGSGGGGGGGGGSETTLTQSPFSLAFAVGDRIITTCRASPGIRNYLAWYQKPKA 180
 DB 118 GGGSGGGGGGGGGSDIQMTQSPSFLASVDRVITTCRASQGINNYLAWYQKPKA 177

CC antirheumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP43990-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention

XX Sequence 248 AA;

Query Match 82.9%; Score 1050; DB 5; Length 248;
 Best Local Similarity 80.6%; Pred. No. 1.4e-66;
 Matches 200; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGVROAPGKLEWVSSISGSRITY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMHVRQAPGKLEWVAVISYDSNKTY 60
 QY 61 ADSVKGRTFTISRDNSKNTLYIQMNSLRADPTAVYCAK-----MDASGYENFPGQTL 114
 DB 61 ADSVKGRTFTISRDNSKNTLYIQMNSLRADPTAVYCARAYDYDILTVGSYFYDYGKGT 120
 QY 115 VTVSSGGGGSGGGSGGGSETTLTQSPFSLAFVGRITTCRASPGIRNLAAYQOKP 174
 DB 121 VTVSSGGGGSGGGSGGGSSDITQMTQSPFTMSASIGDRTITCRASEGIYHMLAWYQOKP 180
 QY 175 GKAPKLLIYAASLTQSGVPSRPSGSGGDTFTLTSSLOPEDFATYYCOQVNSYPLSPFG 234
 DB 181 GKAPKLLIYKASLSLASSGAPSRPSGSGGDTFTLTSSLOPDFAFYCCQVSNYPLTFPG 240
 QY 235 GTRKVEIKR 242
 DB 241 GTRKLEIKR 248

RESULT 15

ID ADG96237 standard; protein; 248 AA.

AC ADG96237;

DT 11-MAR-2004 (first entry)

DE Single chain antibody that immunospecifically binds Blys SeqID 1421.

KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KW B cell proliferation; differentiation; scfv; myasthenia gravis;
 KW multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KW carcinoma; lymphoma; antirheumatic; antiarthritic; neuroprotective;
 KW antinflammatory; antiaesthetic; antiallergic; cytostatic.

OS Unidentified.

PN MO2003055979-AA2.

PD 10-JUL-2003.

PF 14-NOV-2002; 2002WO-US036496.

PR 16-NOV-2001; 2001US-033169P.

PR 19-DEC-2001; 2001US-0340817P.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Ruben SM, Barash SC, Choi GH, Vaughan TJ, Hilbert D;

DR WPI; 2003-505530/47.

PT Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.

PS Example 1; SEQ ID NO 1421; 394pp; English.

XX This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scfvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antirheumatic, antiallergic and cytoprotective.
 CC antinflammatory, antiaesthetic, antiallergic and cytoprotective. This
 CC polypeptide sequence is a single chain antibody that binds Blys of the
 CC invention. NOTE: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 248 AA;

Query Match 82.9%; Score 1050; DB 7; Length 248;
 Best Local Similarity 80.6%; Pred. No. 1.4e-66;
 Matches 200; Conservative 20; Mismatches 22; Indels 6; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGVROAPGKLEWVSSISGSRITY 60
 DB 1 EVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMHVRQAPGKLEWVAVISYDSNKTY 60
 QY 61 ADSVKGRTFTISRDNSKNTLYIQMNSLRADPTAVYCAK-----MDASGYENFPGQTL 114
 DB 61 ADSVKGRTFTISRDNSKNTLYIQMNSLRADPTAVYCARAYDYDILTVGSYFYDYGKGT 120
 QY 115 VTVSSGGGGSGGGSGGGSETTLTQSPFSLAFVGRITTCRASPGIRNLAAYQOKP 174
 DB 121 VTVSSGGGGSGGGSGGGSSDITQMTQSPFTMSASIGDRTITCRASEGIYHMLAWYQOKP 180
 QY 175 GKAPKLLIYAASLTQSGVPSRPSGSGGDTFTLTSSLOPEDFATYYCOQVNSYPLSPFG 234
 DB 181 GKAPKLLIYKASLSLASSGAPSRPSGSGGDTFTLTSSLOPDFAFYCCQVSNYPLTFPG 240
 QY 235 GTRKVEIKR 242
 DB 241 GTRKLEIKR 248

Search completed: April 19, 2005, 16:39:13
 Job time : 122.008 secs

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OM protein - protein search, using SW model

Run on: April 19, 2005, 16:32:47 ; Search time 29.7541 Seconds
(without alignments)
607.146 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267
Sequence: 1 QVQLVESGGGLVQPGGSLRL.....QQYNSTPLSPFGGATKVEIKR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfill1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1057.5	83.5	245	4 US-09-138-091A-76	Sequence 76, Appl
2	1056.5	83.4	245	3 US-08-918-148-78	Sequence 78, Appl
3	1047	82.6	240	4 US-09-192-854-2	Sequence 2, Appl
4	1040.5	82.1	245	3 US-08-918-148-75	Sequence 75, Appl
5	1040.5	82.1	245	4 US-09-138-091A-73	Sequence 73, Appl
6	1002.5	79.1	245	3 US-08-918-148-76	Sequence 76, Appl
7	1002.5	79.1	245	4 US-09-138-091A-74	Sequence 74, Appl
8	1002	79.1	244	3 US-08-918-148-77	Sequence 77, Appl
9	1002	79.1	244	4 US-09-138-091A-75	Sequence 75, Appl
10	937.5	74.0	284	3 US-08-564-164A-2	Sequence 2, Appl
11	921	72.7	301	2 US-08-661-052-14	Sequence 14, Appl
12	921	72.7	301	3 US-09-188-082-14	Sequence 14, Appl
13	921	72.7	301	3 US-09-364-088-14	Sequence 14, Appl
14	921	72.7	301	3 US-09-102-716-14	Sequence 14, Appl
15	921	72.7	553	2 US-08-661-052-16	Sequence 16, Appl
16	921	72.7	553	3 US-09-188-082-16	Sequence 16, Appl
17	921	72.7	553	3 US-09-364-088-16	Sequence 16, Appl
18	921	72.7	553	3 US-09-102-716-16	Sequence 16, Appl
19	914.5	72.2	240	1 US-08-488-113B-148	Sequence 148, App
20	914.5	72.2	240	1 US-08-477-84B-148	Sequence 148, App
21	914.5	72.2	240	2 US-08-646-360-148	Sequence 148, App
22	914.5	72.2	240	3 US-08-839-765-148	Sequence 148, App
23	914.5	72.2	240	3 US-09-136-389-148	Sequence 148, App
24	914.5	72.2	240	3 US-09-610-838-148	Sequence 148, App
25	914.5	72.2	240	4 US-09-711-485-148	Sequence 148, App
26	912	72.0	248	2 US-08-887-352B-23	Sequence 23, Appl
27	912	72.0	248	3 US-09-109-207C-23	Sequence 23, Appl

28	912	72.0	248	3 US-09-296-005-23	Sequence 23, Appl
29	912	72.0	248	4 US-09-920-171-23	Sequence 23, Appl
30	912	72.0	248	4 US-09-716-028-23	Sequence 23, Appl
31	912	72.0	248	4 US-10-113-996-23	Sequence 23, Appl
32	911	71.9	248	2 US-08-887-352B-22	Sequence 22, Appl
33	911	71.9	248	3 US-09-109-207C-22	Sequence 22, Appl
34	911	71.9	248	3 US-09-296-005-22	Sequence 22, Appl
35	911	71.9	248	4 US-09-920-171-22	Sequence 22, Appl
36	911	71.9	248	4 US-09-716-028-22	Sequence 22, Appl
37	911	71.9	248	4 US-10-113-996-22	Sequence 22, Appl
38	909.5	71.8	281	3 US-09-025-769B-178	Sequence 178, App
39	909.5	71.8	281	4 US-09-490-070A-178	Sequence 178, App
40	909.5	71.8	281	4 US-09-490-153-178	Sequence 178, App
41	909.5	71.8	281	4 US-09-490-324-178	Sequence 178, App
42	893.5	70.5	282	2 US-08-860-174A-10	Sequence 10, Appl
43	884	69.8	236	2 US-08-190-199A-65	Sequence 65, Appl
44	873	68.9	255	3 US-09-553-498-8	Sequence 8, Appl
45	873	68.9	255	4 US-09-618-869-8	Sequence 8, Appl

ALIGNMENTS

```
RESULT 1
US-09-138-091A-76
; Sequence 76, Application US/09138091A
; Patent No. 6737249
; GENERAL INFORMATION:
; APPLICANT: Adams, Camellia W.
; APPLICANT: Carter, Paul J.
; APPLICANT: Fendly, Brian M.
; APPLICANT: Gurney, Austin L.
; TITLE OF INVENTION: Agonist Antibodies
; FILE REFERENCE: 9491-013-27
; CURRENT APPLICATION NUMBER: US/09/138,091A
; PRIOR FILING DATE: 1998-08-21
; PRIOR APPLICATION NUMBER: US 60/056,736
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FaSTSeq for Windows Version 4.0
; SEQ ID NO: 76
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: single chain antibody (scFv) fragments
; NAME/KEY: VARIANT
; LOCATION: 208
; OTHER INFORMATION: Xaa = Any Amino Acid
US-09-138-091A-76

Query Match      83.5%; Score 1057.5; DB 4; Length 245;
Best Local Similarity 83.1%; Pred. No. 2.4e-73;
Matches 201; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTPSYAMGVRRAPGKLEWVSISGSSRYYY 60
   |||||
DB 3 QVQLVESGGGLVQPGGSLRLSCAASGFTPSYAMGVRRAPGKLEWVSISGSSRYYY 62
   |||||

QY 61 ADSVKRFTISRDNKNTLYIQNLSLRADTVVYCAKMDAGSYENFGQGLTVVSSG 120
   |||||
DB 63 ADSVKRFTISRDNKNTLYIQNLSLRADTVVYCAR-DRGSTGMDVNGRGLTVVSSG 121
   |||||

QY 121 GGGSGGGSGGGSGSETTLQSPKFLSAFYGDRTITTCRASPGIRNLAVYQKRGAPYL 180
   |||||
DB 122 GGGSGGGSGGGSGSDIQMTQSPKFLSASIGDRVTTCRASPGIRNLAVYQKRGAPYL 181
   |||||

QY 181 LITAASTLQGVPSRFGSGSGTDFLTITSSLOPEDFATYYCOQNSYPLSPFGGATKVEI 240
   |||||
DB 182 LITKASLASGAPSRFGSGSGTDFLTITSSLOPEDFATYYCOQNSYPLSPFGGATKVEI 241
   |||||

QY 241 KR 242
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Db 242 KR 243

RESULT 2

US-08-918-148-78
Sequence 78, Application US/08918148A

Patent No. 6342220

GENERAL INFORMATION:

APPLICANT: Adams, Camellia

APPLICANT: W. Carter, Paul J.

APPLICANT: Gurney, Brian M.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Agonist Antibodies

FILE REFERENCE: P0979

CURRENT APPLICATION NUMBER: US/08/918,148A

CURRENT FILING DATE: 1997-08-25

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 78

LENGTH: 245

TYPE: PRT

ORGANISM: artificial

FEATURE:

NAME/KEY: unknown

LOCATION: 208

OTHER INFORMATION: unknown amino acid

US-08-918-148-78

Query Match 83.4%; Score 1056.5; DB 3; Length 245;

Best Local Similarity 83.1%; Pred. No. 2.9e-73;

Matches 201; Conservative 20; Mismatches 20; Indels 1; Gaps 1;

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

US-09-192-854-2

Query Match 82.6%; Score 1047; DB 4; Length 240;

Best Local Similarity 85.2%; Pred. No. 1.5e-72;

Matches 207; Conservative 11; Mismatches 21; Indels 4; Gaps 2;

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

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Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

RESULT 4

US-08-918-148-75
Sequence 75, Application US/08918148A

Patent No. 6342220

GENERAL INFORMATION:

APPLICANT: Adams, Camellia

APPLICANT: W. Carter, Paul J.

APPLICANT: Gurney, Brian M.

APPLICANT: Gurney, Austin L.

TITLE OF INVENTION: Agonist Antibodies

FILE REFERENCE: P0979

CURRENT APPLICATION NUMBER: US/08/918,148A

CURRENT FILING DATE: 1997-08-25

NUMBER OF SEQ ID NOS: 79

SEQ ID NO 75

LENGTH: 245

TYPE: PRT

ORGANISM: artificial

US-08-918-148-75

Query Match 82.1%; Score 1040.5; DB 3; Length 245;

Best Local Similarity 81.0%; Pred. No. 4.8e-72;

Matches 196; Conservative 20; Mismatches 25; Indels 1; Gaps 1;

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db 242 KR 243

Db	22	IQLVESGGGVVQGRSLRLSSCGSGFIPSDNVMYVWRAPEKGIEMVATISDGSYTYYP	80
Qy	62	DSYKRFITSRNRSKNTLYLQMSLRADPTAVYCAKMDAGSY-----NFPMQGLVLT	116
Db	81	DSYKRFITSRNRSKNTLYLQMSLRADPTAVYCAR---GYRRYGAMDYWGQGIPTV	136
Qy	117	VSSGGGGSGGGSGGGSGGSETTLTQSPSLSAFVGDRLITTCRASPGI-----RNYLAMY	170
Db	137	VSSGGGGSGGGSGGGSGGSDIQLTQSPSLSAFVGDRLITTCRSGSYLVSSNQNYLAMY	196
Qy	171	QQKPGKAPKLLIYAASTLQGYPSRFSSGSGSTDTLTLSLQPEDPATYTCQYNSYPL	230
Db	197	QQKPGKAPKLLIYMASTRSGVPSRFSSGSGSTDTFTLTSLQPEDPATYTCQYLS-SW	255
Qy	231	SFGGKTVEIK 241	
Db	256	TFGGKTVEIK 266	

RESULT 12
US-09-188-082-14

```

1  GENERAL INFORMATION:
2  APPLICANT:  Yashwant M. Deo
3  APPLICANT:  Joel Goldstein
4  APPLICANT:  Robert Graziano
5  APPLICANT:  Chelian Somasundaram
6  TITLE OF INVENTION:  THERAPEUTIC COMPOUNDS COMPRIS
7  TITLE OF INVENTION:  OF ANTI-PC RECEPTOR ANTIBODIES
8  NUMBER OF SEQUENCES:  16
9  CORRESPONDENCE ADDRESS:
10 ADDRESSSEE:  LAHIVE & COCKFIELD
11 STREET:  60 State Street, Suite 510
12 CITY:  Boston
13 STATE:  Massachusetts
14 COUNTRY:  USA
15 ZIP:  02109-1875
16 COMPUTER READABLE FORM:
17 MEDIUM TYPE:  Floppy disk
18 COMPUTER:  IBM PC compatible
19 OPERATING SYSTEM:  PC-DOS/MS-DOS
20 SOFTWARE:  Patent In Release #1.0, Version #1.25
21 CURRENT APPLICATION DATA:
22 APPLICATION NUMBER:  US/09/188,082
23 FILING DATE:
24 PRIOR APPLICATION DATA:
25 APPLICATION NUMBER:  08/661,052
26 FILING DATE:
27 ATTORNEY/AGENT INFORMATION:
28 NAME:  Arnold, Beth E.
29 REGISTRATION NUMBER:  35,430
30 REFERENCE/DOCKET NUMBER:  MX1-043CP
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE:  (617)227-7400
33 TELEFAX:  (617)227-5941
34 INFORMATION FOR SEQ ID NO:  14:
35 SEQUENCE CHARACTERISTICS:
36 LENGTH:  301 amino acids
37 TYPE:  amino acid
38 TOPOLOGY:  linear
39 MOLECULE TYPE:  protein
40 US-09-188-082-14

```

Query Match	72.7%;	Score 921;	DB 3;	Length 301;
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Matches 183; Conservative 20; Mismatches 32; Indels 16; Gaps 4;

QY 62 DSVKGRFTISRDN SKNTLYLQMSLR AEDTAVYYCAKMDASGSY-----FNFWGQGLVT 116

Db 81 DSVKGFRTISRDNSSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQGTPTV 136
QY 117 VSSGGGGGGGGGGGGGGSETTLTQSPSLSAFVGRITITTCASPGI-----RNYLAWY 170
137 VSSGGGGGGGGGGGGGGSDIQLTQSPSSLASVGRVITTCSSQSOSVLYSSNQKNYLA 196
Db 137 VSSGGGGGGGGGGGGGGSDIQLTQSPSSLASVGRVITTCSSQSOSVLYSSNQKNYLA 196
QY 171 OOKPGKAPKLLIYAASLTQSGVPSRPSGSGGTDTFTLTITSSLOPPDPATYYCOQYNSYPL 230
197 OOKPGKAPKLLIYMASTRSGVPSRPSGSGGTDTFTLTITSSLOPPDPATYYCHQYLS-SW 255
QY 231 SFGGKTKEIK 241
Db 256 TFGGKTKEIK 266

RESULT 13

US-09-364-088-14
; Sequence 14, Application US/09364088
; Patent No. 6365161
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo, et al.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD, LLP
; STREET: 28 State Street, 24th Floor
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/364,088
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 09/188,082
; FILING DATE: 07-JUNE-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,172
; FILING DATE: 07-JUNE-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Remillard, Jane E.
; REGISTRATION NUMBER: 38,872
; REFERENCE/DOCKET NUMBER: MXI-043CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)742-7414
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-364-088-14

Query Match 72.7%; Score 921; DB 3; Length 301;
Best Local Similarity 72.9%; Pred. No. 7.8e-63;
Matches 183; Conservative 20; Mismatches 32; Indels 16; Gaps 4;
QY 2 VOLVESGGGLVPGGSLRLSQAASGFTFSSYAMGWROAPGKGLEWVSSISGSSRYIYA 61
1 IOLVESGGGVVPGSLRLSSSSGFIIFBDNTMYWVROAPGKGLEWVATISDGSSTYYP 80
Db 21 IOLVESGGGVVPGSLRLSSSSGFIIFBDNTMYWVROAPGKGLEWVATISDGSSTYYP 80
QY 62 DSVKGFRTISRDNSSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQGTPTV 116
81 DSVKGFRTISRDNSSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQGTPTV 136

QY 117 VSSGGGGGGGGGGGGGGSETTLTQSPSLSAFVGRITITTCASPGI-----RNYLAWY 170
137 VSSGGGGGGGGGGGGGGSDIQLTQSPSSLASVGRVITTCSSQSOSVLYSSNQKNYLA 196
Db 137 VSSGGGGGGGGGGGGGGSDIQLTQSPSSLASVGRVITTCSSQSOSVLYSSNQKNYLA 196
QY 171 OOKPGKAPKLLIYAASLTQSGVPSRPSGSGGTDTFTLTITSSLOPPDPATYYCOQYNSYPL 230
197 OOKPGKAPKLLIYMASTRSGVPSRPSGSGGTDTFTLTITSSLOPPDPATYYCHQYLS-SW 255
QY 231 SFGGKTKEIK 241
Db 256 TFGGKTKEIK 266

RESULT 14

US-09-102-716-14
; Sequence 14, Application US/09102716
; Patent No. 6395272
; GENERAL INFORMATION:
; APPLICANT: Yashwant M. Deo
; Joel Goldstein
; Robert Graziano
; Chehian Somaundaram
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
; OF ANTI-FC RECEPTOR ANTIBODIES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/102,716
; FILING DATE: 22-Jun-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/661,052
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Arnold, Beth E.
; REGISTRATION NUMBER: 35,430
; REFERENCE/DOCKET NUMBER: MXI-043CP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 301 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-09-102-716-14

Query Match 72.7%; Score 921; DB 3; Length 301;
Best Local Similarity 72.9%; Pred. No. 7.8e-63;
Matches 183; Conservative 20; Mismatches 32; Indels 16; Gaps 4;
QY 2 VOLVESGGGLVPGGSLRLSQAASGFTFSSYAMGWROAPGKGLEWVSSISGSSRYIYA 61
1 IOLVESGGGVVPGSLRLSSSSGFIIFBDNTMYWVROAPGKGLEWVATISDGSSTYYP 80
Db 21 IOLVESGGGVVPGSLRLSSSSGFIIFBDNTMYWVROAPGKGLEWVATISDGSSTYYP 80
QY 62 DSVKGFRTISRDNSSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQGTPTV 116
81 DSVKGFRTISRDNSSKNTLFLQMDSLRPEDTGVYFCAR-----GYRYEGAMDYWGQGTPTV 136
QY 117 VSSGGGGGGGGGGGGGGSETTLTQSPSLSAFVGRITITTCASPGI-----RNYLAWY 170

Db 137 VSSGGGGGGGGGGSDIQLTQSPSSLSASVGDRTITCKSGQSVLYSSNOKNYLAWY 196
QY 171 QOKPGKAPKLLIYAASGLTQSGVPSRFGSGSGTDFLTITSLQPEDPATYCCOYNSYPL 230
Db 197 QOKPGKAPKLLIYMASTRSGVPSRFGSGSGTDFLTITSLQPEDPATYCHQYLS-SW 255
QY 231 SFGGKTKVEIK 241
Db 256 TFGGKTKVEIK 266

RESULT 15

US-08-661-052-16
Sequence 16, Application US/08661052
Patent No. 5837243
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Robert Graziano
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/661,052
FILING DATE:
Prior Application DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Arnold, Beth E.
REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-661-052-16

Query Match 72.7%; Score 921; DB 2; Length 553;

Best Local Similarity 72.9%; Pred. No. 1.5e-62; Indels 16; Gaps 4;
Matches 183; Conservative 20; Mismatches 32;

QY 2 VOLVESGGGLVDPGSLRLSCAAGFTFSYANGVROAPGKLEWVSSISGSSRYIYYA 61
Db 21 IQLVESGGGVVQGRSLRLSCSSGFIISDNVYWRQAPGKLEWVATISDGSYTYIP 80
QY 62 DSYKGRFTISRDNKSTLYIQNNSLRAPEDTAVYYCAMDASGSY-----FNFWGGTLVT 116
Db 81 DSYKGRFTISRDNKSTLYIQNNSLRAPEDTAVYYCAMDASGSY-----GYRYEGAMDYWGQGPVT 136
QY 117 VSSGGGGGGGGGGSGSETTLTQSPFLSAPVGDRTITCRASPGI-----RNYLAWY 170
Db 137 VSSGGGGGGGGGGSDIQLTQSPSSLSASVGDRTITCKSGQSVLYSSNOKNYLAWY 196
QY 171 QOKPGKAPKLLIYAASGLTQSGVPSRFGSGSGTDFLTITSLQPEDPATYCCOYNSYPL 230

Db 197 QOKPGKAPKLLIYMASTRSGVPSRFGSGSGTDFLTITSLQPEDPATYCHQYLS-SW 255
QY 231 SFGGKTKVEIK 241
Db 256 TFGGKTKVEIK 266

Search completed: April 19, 2005, 16:45:20
Job time : 30.7541 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 16:43:24 ; Search time 87.2787 Seconds
(without alignments)
921.573 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267
Sequence: 1 QVQLVSGGGLVQPGGSLRL.....QQYNSYPLSGGCTKVEIKR 242

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1421835 seqs, 332370683 residues

Total number of hits satisfying chosen parameters: 1421835

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA.*

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
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18: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
19: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the total being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1267	100.0	242	17	US-10-855-755-2 Sequence 2, Appl1
2	1084.5	85.6	239	17	US-10-935-290-80 Sequence 2, Appl1
3	1069	84.4	291	15	US-10-406-830-10 Sequence 10, Appl1
4	1065.5	84.1	288	9	US-09-818-247-22 Sequence 22, Appl1
5	1060.5	83.7	247	10	US-09-880-748-1923 Sequence 1923, Ap
6	1060.5	83.7	247	15	US-10-293-418-1923 Sequence 1923, Ap
7	1058.5	83.5	239	10	US-09-880-748-1922 Sequence 1922, Ap
8	1058.5	83.5	239	15	US-10-293-418-1922 Sequence 1922, Ap
9	1050.5	82.9	239	10	US-09-880-748-1882 Sequence 1882, Ap
10	1050.5	82.9	239	15	US-10-293-418-1882 Sequence 1882, Ap
11	1050	82.9	248	10	US-09-880-748-1421 Sequence 1421, Ap
12	1050	82.9	248	15	US-10-293-418-1421 Sequence 1421, Ap
13	1047	82.6	240	9	US-09-192-854-2 Sequence 2, Appl1

14	1047	82.6	240	9	US-09-968-561A-2	Sequence 2, Appl1
15	1047	82.6	240	10	US-09-968-744A-2	Sequence 2, Appl1
16	1047	82.6	240	11	US-09-968-561A-2	Sequence 2, Appl1
17	1046	82.6	250	15	US-10-423-847-12	Sequence 12, Appl1
18	1046	82.6	250	17	US-10-831-063-12	Sequence 98, Appl1
19	1044	82.4	240	17	US-10-935-290-98	Sequence 1935, Ap
20	1043.5	82.4	243	10	US-09-880-748-1935	Sequence 1935, Ap
21	1043.5	82.4	243	15	US-10-293-418-1935	Sequence 16, Appl1
22	1041	82.2	249	17	US-10-423-847-16	Sequence 16, Appl1
23	1041	82.2	249	17	US-10-831-063-16	Sequence 15, Appl1
24	1041	82.2	250	15	US-10-423-847-15	Sequence 15, Appl1
25	1041	82.2	250	17	US-10-831-063-15	Sequence 1310, Ap
26	1040.5	82.1	251	10	US-09-880-748-1910	Sequence 1310, Ap
27	1040.5	82.1	251	15	US-10-293-418-1910	Sequence 50, Appl1
28	1040	82.1	241	8	US-08-779-457-50	Sequence 50, Appl1
29	1040	82.1	241	17	US-10-921-710-50	Sequence 9, Appl1
30	1039	82.0	291	15	US-10-406-830-9	Sequence 1945, Ap
31	1033.5	81.6	243	10	US-09-880-748-1945	Sequence 1945, Ap
32	1033.5	81.6	243	15	US-10-293-418-1945	Sequence 82, Appl1
33	1031	81.4	244	10	US-09-880-748-82	Sequence 2005, Ap
34	1031	81.4	244	15	US-10-293-418-82	Sequence 2005, Ap
35	1029.5	81.3	237	10	US-09-880-748-2005	Sequence 1889, Ap
36	1029.5	81.3	237	15	US-10-293-418-2005	Sequence 1901, Ap
37	1029.5	81.3	241	10	US-09-880-748-1889	Sequence 1889, Ap
38	1029.5	81.3	241	15	US-09-880-748-1901	Sequence 1177, Ap
39	1029.5	81.3	241	15	US-10-293-418-1889	Sequence 1177, Ap
40	1029.5	81.3	241	15	US-10-293-418-1901	Sequence 1177, Ap
41	1029.5	81.3	247	10	US-09-880-748-1177	Sequence 1177, Ap
42	1029.5	81.3	247	15	US-10-293-418-1177	Sequence 1177, Ap
43	1027.5	81.1	237	10	US-09-880-748-2114	Sequence 2114, Ap
44	1027.5	81.1	237	15	US-10-293-418-2114	Sequence 164, App
45	1027	81.1	244	10	US-09-880-748-164	

ALIGNMENTS

RESULT 1
US-10-855-755-2
Sequence 2, Application US/10855755
Publication No. US20050037339A1
GENERAL INFORMATION:
APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
APPLICANT: Marks, James D
APPLICANT: Poul, Marie A
APPLICANT: Becerril, Balazar
TITLE OF INVENTION: METHODS OF SELECTING INTERNALIZING ANTIBODIES
FILE REFERENCE: 4070-895011US
CURRENT APPLICATION NUMBER: US/10/855,755
CURRENT FILING DATE: 2004-05-26
PRIOR APPLICATION NUMBER: US 60/082,953
PRIOR FILING DATE: 1998-04-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 242
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Human phage display antibody
FEATURE:
NAME/KEY: SITE
LOCATION: (31)..(35)
OTHER INFORMATION: VH-CDR1
FEATURE:
NAME/KEY: SITE
LOCATION: (50)..(66)
OTHER INFORMATION: VH-CDR2
FEATURE:
NAME/KEY: SITE
LOCATION: (99)..(108)
OTHER INFORMATION: VH-CDR3
FEATURE:

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; NAME/KEY: SITE
; LOCATION: (157)..(167)
; OTHER INFORMATION: VL-CDR1
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (184)..(190)
; OTHER INFORMATION: VL-CDR2
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (223)..(231)
; OTHER INFORMATION: VL-CDR3
US-10-855-755-2

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Query Match      100.0%; Score 1267; DB 17; Length 242;
Best Local Similarity 100.0%; Pred. No. 6.4e-79;
Matches 242; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWSSISGSSRYYY 60
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DB 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWSSISGSSRYYY 60
QY 61 ADSVGRFTISRDNKNTLYLQMSLRADDTAVYCAKADASGYPNFWGQGLTVTVSSG 120
   |||||
DB 61 ADSVGRFTISRDNKNTLYLQMSLRADDTAVYCAKADASGYPNFWGQGLTVTVSSG 120
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
   |||||
DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
QY 122 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
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DB 122 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
QY 181 LIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTVKI 240
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DB 181 LIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTVKI 240
QY 241 KR 242
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DB 241 KR 242

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RESULT 2
US-10-935-290-80
; Sequence 80, Application US/10935290
; Publication No. US20050069542A1
; GENERAL INFORMATION:
; APPLICANT: Baker et al.
; TITLE OF INVENTION: Antibodies that Specifically Bind to GMAD
; FILE REFERENCE: PFS84PI
; CURRENT APPLICATION NUMBER: US/10/935,290
; CURRENT FILING DATE: 2004-09-08
; PRIOR APPLICATION NUMBER: PCT/US03/09625
; PRIOR FILING DATE: 2003-03-28
; PRIOR APPLICATION NUMBER: 60/368,813
; PRIOR FILING DATE: 2002-04-01
; NUMBER OF SEQ ID NOS: 234
; SEQ ID NO 80
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: scfv protein GMBG655
US-10-935-290-80

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Query Match      85.6%; Score 1084.5; DB 17; Length 239;
Best Local Similarity 85.1%; Pred. No. 1.8e-66;
Matches 206; Conservative 16; Mismatches 17; Indels 3; Gaps 1;

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QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWSSISGSSRYYY 60
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DB 1 EVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWSSISGSSRYYY 60
QY 61 ADSVGRFTISRDNKNTLYLQMSLRADDTAVYCAKADASGYPNFWGQGLTVTVSSG 120
   |||||
DB 61 ADSVGRFTISRDNKNTLYLQMSLRADDTAVYCAKADASGYPNFWGQGLTVTVSSG 120
QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
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DB 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
QY 181 LIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTVKI 240
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DB 181 LIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTVKI 240
QY 241 KR 242
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DB 241 KR 242

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QY 121 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 180
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DB 118 GGGSGGGSGGGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 177
QY 181 LIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTVKI 240
   |||||
DB 178 LIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTVKI 237
QY 241 KR 242
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DB 238 KR 239

```

```

RESULT 3
US-10-406-830-10
; Sequence 10, Application US/10406830
; Publication No. US20040071696A1
; GENERAL INFORMATION:
; APPLICANT: ADAMS, GREGORY P.
; APPLICANT: HORAK, EVA M.
; APPLICANT: WEINER, LOUIS M.
; APPLICANT: JAMES, MARKS D.
; TITLE OF INVENTION: BISPECIFIC SINGLE CHAIN Fv ANTIBODY MOLECULES AND METHODS OF USE
; FILE REFERENCE: 407T-000410US
; CURRENT APPLICATION NUMBER: US/10/406,830
; CURRENT FILING DATE: 2003-04-04
; PRIOR APPLICATION NUMBER: US 60/370,276
; PRIOR FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 10
; LENGTH: 291
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Synthetic antibody.
US-10-406-830-10

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Query Match      84.4%; Score 1069; DB 15; Length 291;
Best Local Similarity 84.1%; Pred. No. 2.4e-65;
Matches 207; Conservative 13; Mismatches 22; Indels 4; Gaps 1;

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QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWSSISGSSRYYY 60
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DB 23 QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLEWSSISGSSRYYY 82
QY 61 ADSVGRFTISRDNKNTLYLQMSLRADDTAVYCAKADASG-----YFNWGQGLTVT 116
   |||||
DB 83 ADSVGRFTISRDNKNTLYLQMSLRADDTAVYCAKADASG-----YFNWGQGLTVT 142
QY 117 VSSGGGGSGGGSGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 176
   |||||
DB 143 VSSGGGGSGGGSGSETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQKPKAPKL 202
QY 177 APLKLIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTV 236
   |||||
DB 203 APLKLIYAASLTQSGVPSRFSGSGGTDFLTLLTSSLOPEDPATYYCOQYNSYPLSFGGKTV 262
QY 237 KVEIKR 242
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DB 263 KVEIKR 268

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RESULT 4
US-09-818-247-22
; Sequence 22, Application US/09818247
; Patent No. US20020102657A1
; GENERAL INFORMATION:
; APPLICANT: Mostoy, Keith E.
; APPLICANT: Chapin, Steven J.
; APPLICANT: Richman-Eisenstat, Janice
; APPLICANT: The Regents of the University of California

```

TITLE OF INVENTION: Ligands Directed to the No. US20020102657A1-Secretory Component,
 FILE OF INVENTION: No. US20020102657A1-Stralk Region of p18r and Methods of Use Ther
 FILE REFERENCE: 18062E-00091005
 CURRENT APPLICATION NUMBER: US/09/818,247
 CURRENT FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: WO PCT/US01/09699
 PRIOR FILING DATE: 2001-03-26
 PRIOR APPLICATION NUMBER: US 60/192,197
 PRIOR FILING DATE: 2000-03-27
 PRIOR APPLICATION NUMBER: US 60/192,198
 PRIOR FILING DATE: 2000-03-27
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: Patent In Ver. 2.1
 SEQ ID NO 22
 LENGTH: 288
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial
 OTHER INFORMATION: Sequence: pelb/4AF/myc/6HIS
 US-09-818-247-22

Query Match 84.1%; Score 1065.5; DB 9; Length 288;
 Best Local Similarity 84.8%; Pred. No. 4.1e-65;
 Matches 206; Conservative 12; Mismatches 24; Indels 1; Gaps 1;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRQAPGKLEWVSISGSSRYYY 60
 DB 23 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRQAPGKLEWVSISGSSRYYY 82
 QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAK-MDASGYFNFNGGTLTVAS 119
 DB 83 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKSTVNSGFGFHGGGTLTVAS 142
 QY 120 GGGSGGGSGGGSGGSETTLTQSPFLSAFVGDRITTCRASPGIRNYLAMYQOKPGK 179
 DB 143 GGGSGGGSGGGSGGSEIVLTQSPSTLSASIGDRVITTCRASEGIVHMLAWYQOKPGK 202
 QY 180 LLIYVASTLQSGVPSRFSGSGGTDFTLTSSLPEDPATYVYCOQNSYPLSFGGTYK 239
 DB 203 LLIYKASLSLAVGSPRFSGSGGTDFTLTSSLPEDPATYVYCOQNSYPLSFGGTYK 262
 QY 240 IKR 242
 DB 263 IKR 265

RESULT 5
 US-09-880-748-1923
 ; Sequence 1923, Application US/09880748
 ; Publication No. US2003005937A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruden et al.
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
 ; FILE REFERENCE: PF523
 ; CURRENT APPLICATION NUMBER: US/09/880,748
 ; CURRENT FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-15
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; NUMBER OF SEQ ID NOS: 3239
 ; SOFTWARE: Patent In Ver. 2.0
 ; SEQ ID NO 1923
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens

US-09-880-748-1923

Query Match 83.7%; Score 1060.5; DB 10; Length 247;
 Best Local Similarity 82.2%; Pred. No. 7.8e-65;

Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRQAPGKLEWVSISGSSRYYY 60
 DB 1 EVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRQAPGKLEWVSISGSSRYYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKMDA---SGS--YFNWGGTLY 115
 DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKGNPRSSLYFFDWGRRTV 120
 QY 116 TVSSGGGSGGGSGGSETTLTQSPFLSAFVGDRITTCRASPGIRNYLAMYQOKPG 175
 DB 121 TVSSGGGSGGGSGGSSDIQNTQSPFLSASIGDRVITTCRASGITHRLAMYQOKG 180
 QY 176 KAPKLLIYVASTLQSGVPSRFSGSGGTDFTLTSSLPEDPATYVYCOQNSYPLSFGG 235
 DB 181 KAPKLLIYKASLSLAVGSPRFSGSGGTDFTLTSSLPEDPATYVYCOQNSYPLSFGG 240
 QY 236 TKVEIKR 242
 DB 241 TKLTIKR 247

RESULT 6
 US-10-293-418-1923

; Sequence 1923, Application US/10293418
 ; Publication No. US2003022396A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ruden et al.
 ; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
 ; FILE REFERENCE: PF523P2
 ; CURRENT APPLICATION NUMBER: US/10/293,418
 ; CURRENT FILING DATE: 2002-11-27
 ; PRIOR APPLICATION NUMBER: 60/331,469
 ; PRIOR FILING DATE: 2001-11-16
 ; PRIOR APPLICATION NUMBER: 60/340,817
 ; PRIOR FILING DATE: 2001-12-19
 ; PRIOR APPLICATION NUMBER: 09/880,748
 ; PRIOR FILING DATE: 2001-06-15
 ; PRIOR APPLICATION NUMBER: 60/293,499
 ; PRIOR FILING DATE: 2001-05-25
 ; PRIOR APPLICATION NUMBER: 60/277,379
 ; PRIOR FILING DATE: 2001-03-21
 ; PRIOR APPLICATION NUMBER: 60/276,248
 ; PRIOR FILING DATE: 2001-03-16
 ; PRIOR APPLICATION NUMBER: 60/240,816
 ; PRIOR FILING DATE: 2000-10-17
 ; PRIOR APPLICATION NUMBER: 60/212,210
 ; PRIOR FILING DATE: 2000-06-16
 ; NUMBER OF SEQ ID NOS: 3247
 ; SEQ ID NO 1923
 ; LENGTH: 247
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-293-418-1923

Query Match 83.7%; Score 1060.5; DB 15; Length 247;
 Best Local Similarity 82.2%; Pred. No. 7.8e-65;
 Matches 203; Conservative 20; Mismatches 19; Indels 5; Gaps 2;

QY 1 QVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRQAPGKLEWVSISGSSRYYY 60
 DB 1 EVQLVSGGGLVQPGGSLRLSCAASGFTSSVAMGVRQAPGKLEWVSISGSSRYYY 60
 QY 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKMDA---SGS--YFNWGGTLY 115
 DB 61 ADSVKGRFTISRDNKNTLYLQWNSLRADTAVYYCAKGNPRSSLYFFDWGRRTV 120
 QY 116 TVSSGGGSGGGSGGSETTLTQSPFLSAFVGDRITTCRASPGIRNYLAMYQOKPG 175


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; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1882

Query Match      82.9%; Score 1050.5; DB 10; Length 239;
Best Local Similarity 81.8%; Pred. No. 3.7e-64;
Matches 198; Conservative 23; Mismatches 18; Indels 3; Gaps 1

OY 1 QVOLVEGGGLVQPGSGSLRLSCAASGFTFSSYAMGVNQAQPKGLMEVSSISGSSRYIY 60
DB 1 QVQLVQSGGGLVLPFGSGSLRLSCAASGFTFSSYSMMWVQAQPKGLEIAVAVSSDCAKXKY 60
OY 61 ADVSVGRFTTISDNKNTLYLQMSLRADDTAVYYCAKMDASGSIFNFWGQTLVTYVSSG 120
DB 61 ADVSVGRFTTISDNKNTLYLQMSLRADDTAVYYCAK---TGSGFYDWGRGTLVTYVSSG 117
OY 121 GGGSGGGSGGGSGSETTLTQSPSPFAFYGDRIITTCRASPGRIRYVLAMYQOKPGKAPL 180
DB 118 GGGSGGGSGGGSGSDIQMTQSPSTLSASIGDRVITTCRASESTYHMLMYQOKPGKAPL 177
OY 181 LIYAASLTQSGVSPRFSGSGSGTDTLTLTISLQPEDFATYYCCQYNSYPLSPFGGTKEYI 240
DB 178 LIYKASLSLASGAPSRNFSGSGSGTDTLTLTISLQPPDPATYYCQYNSNPLTRGGSTKLEI 237
OY 241 KR 242
DB 238 KR 239

RESULT 10
US-10-293-418-1882
; Sequence 1882, Application US/10293418
; Publication No. US20030223996A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunosepecifically Bind BlyS
; FILE REFERENCE: PFS23P2
; CURRENT APPLICATION NUMBER: US/10/293,418
; CURRENT FILING DATE: 2002-11-27
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-16
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1882
; LENGTH: 239
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1882

Query Match      82.9%; Score 1050.5; DB 15; Length 239;
Best Local Similarity 81.8%; Pred. No. 3.7e-64;
Matches 198; Conservative 23; Mismatches 18; Indels 3; Gaps 1

OY 1 QVOLVEGGGLVQPGSGSLRLSCAASGFTFSSYAMGVNQAQPKGLMEVSSISGSSRYIY 60
DB 1 QVQLVQSGGGLVLPFGSGSLRLSCAASGFTFSSYSMMWVQAQPKGLEIAVAVSSDCAKXKY 60
OY 61 ADVSVGRFTTISDNKNTLYLQMSLRADDTAVYYCAKMDASGSIFNFWGQTLVTYVSSG 120
DB 61 ADVSVGRFTTISDNKNTLYLQMSLRADDTAVYYCAK---TGSGFYDWGRGTLVTYVSSG 117
OY 121 GGGSGGGSGGGSGSETTLTQSPSPFAFYGDRIITTCRASPGRIRYVLAMYQOKPGKAPL 180
DB 118 GGGSGGGSGGGSGSDIQMTQSPSTLSASIGDRVITTCRASESTYHMLMYQOKPGKAPL 177
OY 181 LIYAASLTQSGVSPRFSGSGSGTDTLTLTISLQPEDFATYYCCQYNSYPLSPFGGTKEYI 240
DB 178 LIYKASLSLASGAPSRNFSGSGSGTDTLTLTISLQPPDPATYYCQYNSNPLTRGGSTKLEI 237
OY 241 KR 242
DB 238 KR 239

```

```

Db      61  ADVSKGRFTTISRDNASKNTVLYLQNMNSLRADDPAAVYYCAK---TGSGFDYMGKGLVTYVSSG  117
Qy      121  GGGGGGGGGGGGGGGSEETTLTQSPSPSLSAFVGRITTTTCASPGIRNYLAWYQOKPKAKRL  180
Db      118  GGGGGGGGGGGGGGGSDIQMTQSPSTLSASIGDRVITTCRASGCIYHMLAWYQOKPKAKRL  177
Qy      181  LTVASASTQSGVPSRFSGSSGCTPFTLTISLQPEDFATYYCCQOYNSYPLSFGGCTKVEI  240
Db      178  LTVASASTLSAPSRFSGSGGTDFTLTISLQPDPAFYTCQOYNSYPLFTGGGTKLEI  237
Qy      241  KR  242
Db      238  KR  239

RESULT 11
US-09-880-748-1421
; Sequence 1421, Application US/09880748
; Publication No. US2003005937A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23
; CURRENT APPLICATION NUMBER: US/09/880,748
; CURRENT FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/212,210
; PRIOR FILING DATE: 2000-06-15
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 3239
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1421
; LENGTH: 248
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1421

Query Match      82.9%; Score 1050; DB 10; Length 248;
Best local Similarity 80.6%; Pred. No. 4,1e-64;
Matches 200; Conservative 20; Mismatches 22; Indels 6; Gaps 1.

Qy      1  QGVLVESGGGLVQPGGSLRLSCAASGFFPSYAMGWRQAPRGKGLEWVSSISGSSRYYY  60
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      1  EVQLVESGGGLVQPGGSLRLSCAASGFFPSYAMHWNAQARGKLEWVAIVSYDGSNRY  60
Qy      61  ADVSKGRFTTISRDNASKNTVLYLQNMNSLRADDPAAVYYCAK-----MDASGSYFNFWGGTL  114
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      61  ADVSKGRFTTISRDNASKNTVLYLQNMNSLRADDPAAVYYCARAYDYDITGSIYFDYWGKTL  120
Qy      115  VTSSGGGGGGGGGGGGGGSEETTLTQSPSPSLSAFVGRITTTTCRASPGIRNYLAWYQOKP  174
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      121  VTSSGGGGGGGGGGGGGGSDIQMTQSPSTMASIGDRVITTCRASGCIYHMLAWYQOKP  180
Qy      175  GKARLLIYAASTQSGVPSRFSGSSGCTDFTLTISLQPEDFATYYCCQOYNSYPLSFGG  234
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db      181  GKARLLIYKASLSLAPSRFSGSGCTDFTLTISLQPDPAFYTCQOYNSYPLFTGGG  240
Qy      235  GTKVEIKR  242
      || : |||
Db      241  GTKLEIKR  248

```


Db 178 LLIYAASLIQSGVPSRFGSGGTDFTLLTISLQPEDFATYYCQGSYSTPNTFGGTKE 237
QY 240 IKR 242
|||
Db 238 IKR 240

RESULT 15
US-09-968-744A-2
; Sequence 2, Application US/09968744A
; Publication No. US20030148372A1
; GENERAL INFORMATION:
; APPLICANT: Tomlinson, Ian M
; APPLICANT: Winter, Gregory
; TITLE OF INVENTION: Method to Screen Phage Display Libraries with Different Ligands
; FILE REFERENCE: 8039/1073
; CURRENT APPLICATION NUMBER: US/09/968,744A
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: GB 9722131.1
; PRIOR FILING DATE: 1997-10-20
; PRIOR APPLICATION NUMBER: US 60/065,248
; PRIOR FILING DATE: 1997-11-13
; PRIOR APPLICATION NUMBER: US 60/066,729
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: PCT/GB98/03135
; PRIOR FILING DATE: 1998-10-20
; PRIOR APPLICATION NUMBER: US 09/511,939
; PRIOR FILING DATE: 2000-02-24
; NUMBER OF SEQ ID NOS: 350
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-968-744A-2

Query Match 82.6%; Score 1047; DB 10; Length 240;
Best Local Similarity 85.2%; Pred. No. 6,4e-64;
Matches 207; Conservative 11; Mismatches 21; Indels 4; Gaps 2;
QY 1 QVQVLSGGGLVPGGSLRLISCAAGFTFSYAMGWYRQAPGKLEWVSSISGSRITYY 60
:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 1 EVQLVESGGGLVQPGGSLRLISCAAGFTFSYAMSWYRQAPGKLEWVSAISGSGSTYY 60
61 ADSVKGRFTISRDNKNTLYLQKNSLRPEDTAVYYCAKMDASGYFNPWGQGLTVYSSG 120
|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 61 ADSVKGRFTISRDNKNTLYLQKNSLRPEDTAVYYCAKMDASGYFNPWGQGLTVYSSG 117
QY 121 GGGSGGGSGGGSGS-ETTLTQSPFLSAFYGDRITTCRASPGIRNYLAWYQOKPGKAPK 179
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 118 GGGSGGGSGGGSGSTIQMTQSPSSLSASVGDRAVITTCRASQSSISYLNWYQOKPGKAPK 177
QY 180 LLIYAASLIQSGVPSRFGSGGTDFTLLTISLQPEDFATYYCQGSYSTPNTFGGTKE 239
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||
Db 178 LLIYAASLIQSGVPSRFGSGGTDFTLLTISLQPEDFATYYCQGSYSTPNTFGGTKE 237
QY 240 IKR 242
|||
Db 238 IKR 240

Search completed: April 19, 2005, 17:00:53
Job time : 88.2787 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: April 19, 2005, 16:32:07 ; Search time 27.2746 Seconds

(without alignments)
853.705 Million cell updates/sec

Title: US-09-250-056B-2

Perfect score: 1267

Sequence: 1 QVQLVSGGGLVQPGGSLRL.....QQYNISYPLSFSGGTKEIKR 242

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	717	56.6	268	A56446	Ig heavy chain V r
2	701.5	55.4	249	S41374	single chain Fv an
3	628.5	49.6	233	UC5322	p53 specific singl
4	540	42.6	119	S31107	Ig heavy chain - h
5	534	42.1	119	C36005	Ig heavy chain V r
6	533	42.1	119	D36005	Ig heavy chain V r
7	526	41.5	138	S31666	Ig heavy chain V r
8	524.5	41.4	141	S31669	Ig heavy chain V r
9	524	41.4	125	S31051	Ig heavy chain V r
10	523	41.3	119	S31108	Ig heavy chain - h
11	522	41.3	127	S38489	Ig heavy chain - h
12	522	41.2	140	S31686	Ig heavy chain V r
13	520	40.0	140	S31588	Ig heavy chain V r
14	517.5	40.8	120	S48798	Ig heavy chain V r
15	517	40.8	123	S31114	Ig heavy chain - h
16	517	40.8	124	S05271	Ig heavy chain pre
17	512.5	40.4	124	S20782	Ig heavy chain V r
18	507	40.0	133	S23624	Ig heavy chain V r
19	505	39.9	135	S31598	Ig heavy chain V r
20	504.5	39.8	140	S70442	Ig heavy chain pre
21	502.5	39.7	122	S20772	Ig heavy chain V r
22	502	39.6	121	I55673	Ig heavy chain - h
23	500.5	39.5	120	S44111	Ig heavy chain V-D
24	499.5	39.4	114	S41120	Ig heavy chain - h
25	499.5	39.4	128	S26790	Ig heavy chain V r
26	498	39.3	132	S40334	Ig kappa chain - h
27	497	39.2	121	S19666	Ig heavy chain V r
28	496	39.1	109	PH1649	Ig heavy chain V r
29	495	39.1	134	S31699	Ig heavy chain V r

30	494.5	39.0	112	2	PH1647	Ig heavy chain V r
31	494	39.0	121	2	F36005	Ig heavy chain V r
32	493	38.9	119	2	F36005	Ig heavy chain V r
33	493	38.9	120	2	S36278	Ig heavy chain V r
34	491.5	38.8	147	2	I37780	Ig variable region
35	491	38.8	117	2	S34012	Ig heavy chain V r
36	490.5	38.7	118	2	S31105	Ig heavy chain (su
37	490.5	38.7	128	2	S26786	Ig heavy chain V r
38	490.5	38.7	151	2	A60943	Ig heavy chain pre
39	490	38.7	123	2	S26794	Ig heavy chain V r
40	490	38.7	139	2	I37781	Ig variable region
41	489	38.6	121	2	S31104	Ig heavy chain (su
42	488	38.5	108	2	S19674	Ig kappa chain V r
43	488	38.5	127	2	S19878	Ig heavy chain V r
44	488	38.5	134	2	S31679	Ig heavy chain V r
45	487.5	38.5	122	2	S31117	Ig heavy chain - h

ALIGNMENTS

RESULT 1

A56446
Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C)

C/Species: Mus musculus (house mouse)

C/Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996

C/Accession: A56446

R/Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.

J. Biol. Chem. 270, 7829-7835, 1995

A/Title: A high affinity digoxin-binding protein displayed on M13 is functionally ident

A/Reference number: A56446; PMID:95229583; PMID:7713873

A/Accession: A56446

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-268 <TAN>

A/Cross-references: GB:020617

C/Keywords: heterotrimer; immunoglobulin

Query Match 56.6%; Score 717; DB 2; Length 268;

Best Local Similarity 56.2%; Pred. No. 4.6e-44;

Matches 136; Conservative 40; Mismatches 64; Indels 2; Gaps 2;

QY	1	QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLRWSSISGSRYYV	60
DB	3	QVQLVSGGGLVQPGGSLRLSCAASGFTSSYAMGVRAQPKGLRWSSISGSRYYV	62
QY	61	ADSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYCAKMDASGYFNFVGGTLVTVSSG	120
DB	63	DPKFGKATTAADTSSNTAVLQLSLTSEDTAVYCAASYLT-RYENYMGQGTIVVSSG	121
QY	121	GGSGGGSGGGSGGSETTLQSPFLSAFVGDRTITICRASPGIRNYLAWYQKRGKAPKL	180
DB	122	GGSGGGSGGGSGGSDIELTQSPFLVSAFVGDRTITICRASPGIRNYLAWYQKRGKAPKL	180
QY	181	LIVAASTLQSGVPSRFRSGSGGTFTLTISLQPEDFATYYCCQVNSYPLSFGGTKEVI	240
DB	181	WVYITHLPPGVAVRARSFGSGSGSYLTISLMGDEDAATYYCCQVNSYPLSFGGTKEVI	240
QY	241	KR 242	
DB	241	KR 242	

RESULT 2

S41374
single chain Fv antibody - mouse

C/Species: Mus musculus (house mouse)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-Jan-1995

C/Accession: S41374

R/Artsemeno, O.; Weller, E.W.; Muentz, K.; Conrad, U.

submitted to the EMBL Data Library, January 1994

A/Description: Construction and functional characterization of a single chain Fv antibo

A/Accession: S41374
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-249 <ART>
A/Cross-references: EMBL:Z29480

Query Match	55.4%	Score 701.5;	DB 2;	Length 249;
Best Local Similarity	53.4%;	Pred. No. 5.4e-43;		
Matches 132;	Conservative 41;	Mismatches 69;	Indels 5;	Gaps 1

```

QY 1 QVQLVESGGGLVQPGGSLTELSCAASGFTTSSYAMGVRAQPGKGLHWSSISGSSRYIY 60
Dy 1 QVQLQSGAGELVIRPQASVTLCTAASFNNKDDYIHVVKQRPKGLMIARIAPASGVKY 60
QY 61 ADSVKGRTISHDNKNTLYIQMNSLRAPEDTAVYYCAKMDASGSYFNPMWGQLVTVSSG 120
Dy 61 VPRFDKKATITADTSSNNTAYLLSLTSLSBTDPAVYYCARBDLTVTSLGWQGGSTVWSR 120
QY 121 GGGSGGGSGGGSGSETTLTQSPSFLSAFVGDRTITICRASPGL-----RNYLAMYQOKPG 175
Dy 121 GGGSGGGSGGGSGSDIELTQSPSPVVAVIPGESVISICRSKSKLLYSDGDSYLEFWLQRPG 180
QY 176 KAPKLLIYAASLTQSGVSPRFSGSGGTFTLTLSIQPEDFAFYVCOQVNSYPLSPFGGG 235
Dy 181 QSPQLLITRMSTLASSGPDPRFSGSGGTFTLTIRISVNEADVGVIYCMQHRERFPLTFGAG 240

```

RESULT 3
JC5322
p53 specific single-chain antibody Pab421 - human

C:Date: 15-May-1997 #sequence_revision 15-May-1997 #text_change 18-Jul-1997
C:Accession: UC5322
R:Jannoc, C.B.; Hyner, N.E.
Biochem. Biophys. Res. Commun. 230, 242-246, 1997
A:Title: Characterization of scFv-421, a single-chain antibody targeted to p53.
A:Reference number: UC5322; MUID: 97168950; PMID: 9016757
A:Accession: UC5322
A:Molecule type: mRNA
A:Residues: 1-233 <JAN>
A:Experimental source: hydridcloma cell
C:Comment: This protein specifically binds the tumor suppressor protein p53. It restores

RESULT 4
S31107
Ig heavy chain - human
C:Species: Homo sapiens (man)
I:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #next_change 17-Mar-1999

R.Accession: S31107
R.Raaphorst, F.M.; Timmers, E.; Kenter, M.J.H.; van Tol, M.J.D.; Voosen, J.M.; Schuurman
Eur. J. Immunol. 22: 247-251, 1992
A.Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple
A.Reference number: S31104; MUID:92111633; PMID:1730252
A.Accession: S31107
A.Status: preliminary; nucleic acid sequence not shown; translation not shown
A.Molecule type: mRNA
A.Residues: 1-119 <RAA>
A.Cross-references: EMBL:X62955
A.Note: The nucleotide sequence was submitted to the EMBL Data Library, October 1991
C.Superfamily: immunoglobulin V region; immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
P.15-98/Domain: immunoglobulin homology <Imm>

Query Match	42.6%;	Score 540;	DB 2;	Length 119;
Best Local Similarity	-87.4%;	Pred. No. 7.5e-32;		
Matches 104; Conservative	5;	Mismatches 10;	Indels 0;	Gaps 0

[illegible]

```

RESULT 5
C36005
Ig heavy chain V region (30p1) - human
C|Species: Homo sapiens (man)
C|Date: 21-Dec-1990 #sequence_revision 21-Dec-1990 #text_change 16-Aug-1996
C|Accession: C36005
R|Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A|Title: Preferential utilization of conserved immunoglobulin heavy chain variable genes
A|Reference number: A36005; MUID:90349571; PMID:211723
A|Accession: C36005
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-119 <SCH>
A|Cross-references: GB:M18513
C|Superfamily: immunoglobulin V region; immunoglobulin homology
C|Keywords: heterodimer; immunoglobulin
F|15-98/Domain: immunoglobulin homology <IMM>

```

Query Match	42.1%;	Score 534;	DB 2;	Length 119;
Best Local Similarity	87.4%;	Pred. No. 2e-31;		
Matches 104;	Conservative	5;	Mismatches 10;	Indels 0; Gaps
Oy	1 QVQLVESGGGLVPGGSLRLSCAASGFTFSYMYGMWRAPQKGLEWYSSIGSGRYY	60		
	:::::			
Db	1 EVQLLEGGGGLVPPGSSLRLSCAASGFTTSSIMSWVRQAPEGKLEWYSALISGSGSTYY	60		
Oy	61 ADSVKGRFTISRDNKNTLYIQMNSLRADETAVYYCAKMDAGSYENFEGGDTLVTS	119		
Db	61 ADSVKGRFTISRDNKNTLYIQMNSLRADETAVYYCAKMDAGSGEDYMGGDTLVTS	119		

RESULT 6
D36005
Ig heavy chain V region (M43) - human
C|Species: Homo sapiens (man)
C|Date: 21-Dec-1990 #sequence
C|Accession: D36005
R|Schroeder Jr., H.W.; Wang, J.Y.
Proc. Natl. Acad. Sci. U.S.A. 87, 6146-6150, 1990
A|Title: Preferential utilization of conserved immunoglobulin heavy chain variable gene
A|Reference number: A36005; MUID:90349571; PMID:2117273
A|Accession: D36005
A|Status: preliminary
A|Molecule type: mRNA

[illegible]

```

RESULT 11
S38489      Ig heavy chain - human (fragment)
C1:Species: Homo sapiens (man)
C1:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 23-Jul-1999
C1:Accession: S38489
R1:Marks, J.D.; Ouweland, W.H.; Bye, J.M.; Finern, R.; Gorick, B.D.; Voak, D.; Thorpe, S.
      submitted to the EMBL Data library, June 1993
A1:Description: Human antibody fragments specific for human blood group antigens from a P
A1:Reference number: S38488
A1:Accession: S38489
A1:Status: preliminary
A1:Molecule type: DNA
A1:Residues: 1-127 <MAR>
A1:Cross-references: EMBL:Z23028, NID:g414025, PIDN:CAA00563.1, PID:g414026
C1:Superfamily: Immunoglobulin V region, immunoglobulin homology
C1:Keywords: heterotetramer; immunoglobulin
F1:5-98/Domain: immunoglobulin homology <IM>

```

Query Match	41.3%	Score 523	DB 2	Length 127
Best Local Similarity	81.9%	Pred. No. 1.3e-30		
Matches 104	Conservative 6	Mismatches 7	Indels 10	Gaps 2
QY	1 QVLTVESGGGLVOPGGSRLRLSCAAGFTFFSSYAMGWRQAPKGLIEWVSISGSSRRYYT	60		
	: : : : : : : : : :			
Db	1 QVQLVQSGGSGGVVQPGGSLRLISCAASGFTFFSSYAMSWVRQAPKGLIEWSAISGGGGSTYY	60		
	: : : : : : : : :			
QY	61 ADSVKGRTTISRDNKNTLLYLOMNSLRADPTAVYYCAK-----MDASGSY-FNFWG	110		
	: : : : : : : : :			
Db	61 ADSVKGRTTISRDNKNTLLYLOMNSLRADPTAVYYCAKSGFPFASDYDSGGYSFDYWG	120		
	: : : : : : : : :			
QY	111 QGTLVTY	117		
Db	121 QGTLVTY	127		

RESULT 12
S31686
Ig heavy chain V region - human (fragment)
C.Species: Homo sapiens (man)
C.Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C.Accession: S31686
R.Cusinier, A.M.; Gauthier, L.; Boubli, L.; Fougereau, M.; Tonnelie, C.
Submitted to the EMBL Data Library, June 1992
A.Description: Mechanisms that generate human immunoglobulin diversity operate from the
A.Reference number: S31585
A.Accession: S31686
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-140 <CUI>
A.Cross-References: EMBL:Z14205, NID:g30966, PIDN:CAA78574.1, PID:g30970
C.Superfamily: Immunoglobulin V region, immunoglobulin homology
C.Keywords: heterotetramer; immunoglobulin
F.34-117/Dmain: immunoglobulin homology <IM>

Query Match	41.2%;	Score 522;	DB 2;	Length 140;
Best Local Similarity	84.3%;	Pred. No. 1.7e-30;		
Matches 102;	Conservative 7;	Mismatches 10;	Indels 2;	Gaps 1;

Db 20 EVQLLESGGGLVQPGGSLRLISCAASGFTTSSYAMSVRQAPGKLEWVSAISGGSGSTYY 79
QY 61 ADSVAGRTTISRDNKNLTLYLQMSLRADDTAVYTCARMDAGS--YENFNGGTLVTVS 118
Db 80 SDVSVAGRTTISRDNKNLTLYLQMSLRADDTAVYTCARPFAGGSPSPDYMGGTLVTVS 139
QY 119 S 119
Db 140 S 140

```

RESULT 13
S31588
Ig heavy chain V region - human (Fragment)
C|Species: Homo sapiens (man)
C|Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 23-Jul-1999
C|Accession: S31588
R|Cusinier, A.M.; Gauthier, L.; Boublil, L.; Fougereau, M.; Tonnelie, C.
submitted to the EMBL Data library, June 1992
A|Description: Mechanisms that generate human immunoglobulin diversity operate from the
A|Reference number: S31585
A|Accession: S31588
A|Status: preliminary
A|Molecule type: mRNA
A|Residues: 1-140 <CUT>
A|Cross-references: EMBL_Z14200, NID:g30957, PIDN:CA476569.1, PID:g30958
C|Superfamily: Immunoglobulin V region, immunoglobulin homology
C|Keywords: heterotetramer; immunoglobulin
F|34-117|Domain: immunoglobulin homology <IMM>

```

[illegible]

RESULT 14
S48798
Ig heavy chain V region (anti-Sm, VH3/Dxp4/JH4b) - human
C.Species: Homo sapiens (man)
C.Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 23-Jul-1999
C.Accession: S48798
R.Mahmoudi, M.; Edwards, J.; Cairns, E.; Bell, D.
submitted to the EMBL Data Library, October 1994
A.Description: Molecular Characterization of natural human anti-Sm autoantibodies.
A.Reference number: S48797
A.Accession: S48798
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-120 <MAH>
A.Cross-references: EMBL, Z46382, NTD:G562324, PIDD:CAA6521.1, PIDD:G1340167
C.Superfamily: Immunoglobulin V region, Immunoglobulin homology
C.Keywords: heterotrimer, Immunoglobulin
F.15-98/Domain: Immunoglobulin homology <IMM>

	Query Match	40.8%	Score 517.5;	DB 2;	Length 120;
	Best Local Similarity	85.8%;	Pred. No. 3e-30;		
	Matches 103; Conservative	5;	Mismatches	11;	Indels 1;
Gy	1 QVQLVESGGGLVPGGSLRLCSAAGFFPSYAMGWNAQPKGLHWISISGSRRYYX	60			
	: :: :	:: ::	:: ::	:: ::	:: ::

Db 1 EVQLLESGGGLVQPGGSLRLISCAASGFTFSYAMSWVRQAPGKLEWNSAISGGSGSTYY 60
 QY 61 ADSVKGRFTISRDNSTKNTLYLQWNSLRAEDTAVYYCAKMDASGS-YENFWGGTLVTVSS 119
 Db 61 ADSVKGRFTISRDNSTKNTLYLQWNSLRAEDTAVYYCAKMDASGS-YENFWGGTLVTVSS 120

RESULT 15

S3114

Ig heavy chain - human

C:Species: Homo sapiens (man)

C:Date: 02-Dec-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C:Accession: S3114

R:Raaphorst, F.M.; Timmer, E.; Kenter, M.J.H.; van Tol, M.J.D.; Vossen, J.M.; Schuurman

Eur. J. Immunol. 22, 247-251, 1992

A:Title: Restricted utilization of germ-line V(H)3 genes and short diverse third comple

A:Reference number: S31104; NCID:9211633; PMID:1730252

A:Accession: S3114

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: mRNA

A:Residues: 1-123 <RAA>

A:Cross-references: EMBL:X62963

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, October 1991

C:Superfamily: immunoglobulin V region; immunoglobulin homology

C:Keywords: heterotetramer; immunoglobulin

F:15-98/Domain: immunoglobulin homology <IMM>

Query Match 40.8%; Score 517; DB 2; Length 123;

Best Local Similarity 82.9%; Pred. No. 3.4e-30;

Matches 102; Conservative 6; Mismatches 11; Indels 4; Gaps 1;

QY 1 QVQLVESGGGLVQPGGSLRLISCAASGFTFSYAMGWVRQAPGKLEWNSISGSSRYIYY 60
 Db 1 EVQLLESGGGLVQPGGSLRLISCAASGFTFSYAMSWVRQAPGKLEWNSAISGGSGSTYY 60
 QY 61 ADSVKGRFTISRDNSTKNTLYLQWNSLRAEDTAVYYCAKMDASGSY---FENFWGGTLVT 116
 Db 61 ADSVKGRFTISRDNSTKNTLYLQWNSLRAEDTAVYYCAKASLYLRFLFWLFDYWGQGTLYVT 120
 QY 117 VSS 119
 Db 121 VSS 123

Search completed: April 19, 2005, 16:44:13
 Job time : 28.2746 secs

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Db 239 KR 240

RESULT 2

ID Q6KB05 PRELIMINARY; PRT; 255 AA.
 AC Q6KB05;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE SCFV B85 protein (Fragment).
 GN Name=SCFV B85;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 RX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Balb/c;
 RA Peter J.C., Wallukat G., Tugler J., Maurice D., Roegel J.C.,
 RI Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; A4746180; CAG34081.1; -.
 DR HSSP; P01837; 1KCR.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00409; Ig_2.
 DR SMART; SM00406; IgV_2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 255 AA; 27445 MW; B68BD38395DP713B CRC64;
 Query Match 70.5%; Score 893; DB 2; Length 255;
 Best Local Similarity 66.3%; Pred. No. 9.8e-63;
 Matches 167; Conservative 36; Mismatches 35; Indels 14; Gaps 3;
 QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGWVROAPGKLEWVSSIGSSRYYY 60
 Db 1 QVQLQSGGGLVAPGGSLKSCAASGFTFSYGMVWRQAPGRLEVAITISGGSYTY 60
 QY 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAPETAVYYCA-----KMDASGSYFNWGGTLY 115
 Db 61 PDSVKGRFTISRDNAKNTLYLQMSLSKEDTAMYYCARHINYYDGA---FDYWGQGTLL 117
 QY 116 TVSSGGSGSGSGSGSGSETTLQSPFSAFVGDRITTCRASPGI-----RNYLAW 169
 Db 118 TVSSGGSGSGSGSGSGSDIYVAQSPSSLSVSAQKVIWMSKSSQSLNSRNQKNTLAW 177
 QY 170 YQQKPGKAPKLLIYAASLTQSGVPSRPSGSGGTDTFTLTISLQPEDPATYYCOQYNSTP 229
 Db 178 YQQKPGGSPKLLIYGASTRSGVPSRPSGSGGTDTFTLTISLQPEDPATYYCOQNHSTP 237
 QY 230 LSTGGTKVAIK 241
 Db 238 LTFGAGTKLEIK 249
 RESULT 3
 QY Q9QYF0 PRELIMINARY; PRT; 238 AA.
 AC Q9QYF0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE CN 8 single chain antibody.
 GN Name=CN 8 scFv;
 OS synthetic construct.
 OC other sequences; artificial sequences.
 RX NCBI_TaxID=32630;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=20183931; PubMed=10706631; DOI=10.1073/pnas.050582197;

RA Shinohara N., Demura T., Fukuda H.;
 RT "Isolation of a vascular cell wall-specific monoclonal antibody
 RT recognizing a cell polarity by using a phase display subtraction
 RT method.";
 RL Proc. Natl. Acad. Sci. U.S.A. 97:2585-2590 (2000).
 DR EMBL; AB036341; BAA88633.1; -.
 DR F01; A33933; A33933.
 DR F01; S19112; S19112.
 DR HSSP; P01820; 1A70.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR SMART; SM00406; IgV_2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 SQ SEQUENCE 298 AA; 31867 MW; E0F968BA17004317 CRC64;

Query Match 69.0%; Score 874.5; DB 2; Length 298;
 Best Local Similarity 67.8%; Pred. No. 3.4e-61;
 Matches 166; Conservative 31; Mismatches 41; Indels 7; Gaps 2;

QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTFSYAMGWVROAPGKLEWVSSIGSSRYYY 60
 Db 40 QVQLQSGGGLVAPGGSLKSCAASGSDPSRYWMSVWRQAPGKLEWIGEINPDSSTINY 99
 QY 61 ADSVKGRFTISRDNSKNTLYLQMNSLRAPETAVYYCAKMDASGSYFN---FNGGGTLYTY 117
 Db 100 TPSLKDRTISRDNAKNTLYLQMSKVRSEDTALYYCAR---ASYGSAVWGQGTLYTY 155
 QY 118 SSGGGSGSGSGSGSGSETTLQSPFSAFVGDRITTCRASPGIRNYLAWYQKPGRA 177
 Db 156 SSGGGSGSGSGSGSGSDIELTQSPASLSASGIVTITCRASGNHNTLAWYQKQGS 215
 QY 178 PKLLIYAASLTQSGVPSRPSGSGGTDTFTLTISLQPEDPATYYCOQYNSTP 237
 Db 216 POLVYNATLADGVPSRPSGSGGTQYSLKINSIQPEDFGSYCOHFTTPTTFGGGTR 275
 QY 238 VEIKR 242
 Db 276 LEIKR 280
 RESULT 4
 ID Q65ZC8 PRELIMINARY; PRT; 244 AA.
 AC Q65ZC8;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE Single-chain Fv (Fragment).
 GN Name=scFv;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 RX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=97362799; PubMed=9219263;
 RA Kontermann R.E., Wing M.G., Winter G.;
 RT "Complement recruitment using bispecific diabodies.";
 RL Nat. Biotechnol. 15:629-631 (1997).
 DR EMBL; Y13057; CAA73500.1; -.
 DR InterPro; IPR003599; Ig.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00409; Ig_2.
 DR SMART; SM00406; IgV_2.
 DR PROSITE; PSS0835; IG_LIKE; 2.
 FT NON TER 1
 SQ SEQUENCE 244 AA; 26127 MW; 4B1F17868338F2BF CRC64;
 Query Match 68.2%; Score 864; DB 2; Length 244;
 Best Local Similarity 66.5%; Pred. No. 1.8e-60;

Matches 163; Conservative 39; Mismatches 39; Indels 4; Gaps 2;

QY 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTSSYAMGWROAPGKLEWVSISGSSRYIY 60
 DB 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTSSYAMGWROAPGKLEWVSISGSSRYIY 60

QY 61 ADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYYCAKMDASGSY--FNFMGGTLVTY 117
 DB 61 AGRFQGRVMTNRTDTSIAAYMEVSRLRSDPTAVYYCAR-EGTGSALYGMQDVGGLVTY 119

QY 118 SSGGGSGGGSGGGSGGGSETTLTQSPFLSAFVGDRTITTCRAPGIRNLIAMVQKRGKA 177
 DB 120 SSGGGSGGGSGGGSGGGSDIQMTQSPSLTSLASIDRVTITTCRAPSEGIYHMLAMVQKRGKA 179

QY 178 PKLLIYAASLTQSGVPSRFSFGSGGTDFLTITSLQPEPATYCCQYNSYPLSPFGGCTK 237
 DB 180 PKFLIYKASLSLGSAPSRFSGSGGTDFLTITSLQPDPAITYCCQYNSYPLSPFGGCTK 239

QY 238 VEIKR 242
 DB 240 LEIKR 244

RESULT 5
 ID 065207 PRELIMINARY; PRT; 248 AA.

AC 065207;
 DT 25-OCT-2004 (T-EMBLrel. 28, Created)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (T-EMBLrel. 28, Last annotation update)
 DE B3(Fv)-PE40 (Fragment).
 GN Name=B3 (Fv)-PE40;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBL_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92020904; PubMed=1924323;
 RA Britkman U., Pai L.H., Fitzgerald D.J., Willingham M., Pastan I.,
 RT "B3(Fv)-P38KDEL, a single-chain immunotoxin that causes complete
 RT regression of a human carcinoma in mice."
 RL Proc. Natl. Acad. Sci. U.S.A. 88:8616-8620(1991).
 DR EMBL; S57990; AAB1971.2; -.
 DR InterPro; IPR003599; Ig_2.
 DR InterPro; IPR007110; Ig_Like.
 DR InterPro; IPR003596; Ig_V.
 DR Pfam; PF00047; Ig_2.
 DR SMART; SM00409; Ig; 2.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 FT NON_TER 248 248
 FT SEQUENCE 248 AA; 26634 MW; 7A3759B43E570950 CRC64;

Query Match 64.4%; Score 815.5; DB 2; Length 248;
 Best Local Similarity 64.5%; Pred. No. 1.3e-56;
 Matches 158; Conservative 29; Mismatches 53; Indels 5; Gaps 1;

QY 2 VOLVESGGGLVOPGSGSLRLSCAASGFTSSYAMGWROAPGKLEWVSISGSSRYIY 61
 DB 3 VKLVESGGGLVOPGSGSLRLSCAASGFTSSYAMGWROAPGKLEWVSISGSSRYIY 62

QY 62 DSVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKMDASGSYFNPWGCTLVTVSSG 121
 DB 63 DTVKGRFTISRDNSKNTLYLQMNSLRAEDTAVYYCAKMDASGSYFNPWGCTLVTVSSG 122

QY 122 GSGGGSGGGSGGGSETTLTQSPFLSAFVGDRTITTCRAPSGI-----RNLIAMVQKRGK 176
 DB 123 GSGGGSGGGSGGGSDVMTQSPSLPLPSLQDQASISCRSSGIYIHSNGNTLYLQKPGQ 182

QY 177 APFLIYAASLTQSGVPSRFSFGSGGTDFLTITSLQPEPATYCCQYNSYPLSPFGGCT 236
 DB 183 SPFLIYKASLSLGSAPSRFSGSGGTDFLTITSLQPDPAITYCCQYNSYPLSPFGGCT 242

QY 237 KVEIK 241
 DB 243 KLEIK 247

RESULT 6
 ID 0921A6 PRELIMINARY; PRT; 241 AA.

AC 0921A6;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE Anti-CEA 79 single chain Fv (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBL_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=98170165; PubMed=9509426;
 RA Chung J.H., Choi S.J., Kim H.J., Kim I.J., Choi I.H., Lee S.D.,
 RA Yi K.S., Sun P.G., Ryu S.H., Chung H.K.,
 RT "Cloning and characterization of cDNAs encoding VH and VL of a
 RT monoclonal anti-CEA antibody (CEA 79) cross-reactive with NCA-95 and
 RT generation of a single-chain Fv molecule (scFv)."
 RL Mol. Cells 7:816-819(1997).
 DR EMBL; U88067; AAB48044.1; -.
 DR PIR; S19965; S19965.
 DR PIR; S19967; S19967.
 DR PIR; S19968; S19968.
 DR PIR; S26325; S26325.
 DR HSSP; P01607; IBMW.
 DR SMART; SM00406; IGV; 2.
 DR PROSITE; PS50835; IG_LIKE; 2.
 FT NON_TER 241 241
 FT SEQUENCE 241 AA; 26086 MW; 0276887248B9C771 CRC64;

Query Match 58.8%; Score 745; DB 2; Length 241;
 Best Local Similarity 57.7%; Pred. No. 4.7e-51;
 Matches 142; Conservative 42; Mismatches 52; Indels 10; Gaps 4;

QY 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTSSYAMGWROAPGKLEWVSISGSSRYIY 60
 DB 1 QVQLVSGGGLVOPGSGSLRLSCAASGFTSSYAMGWROAPGKLEWVSISGSSRYIY 60

QY 61 ADSVKGRTISRDNSKNTLYLQMNSLRAEDTAVYYCAKMDASGSYFNPWGCTLVTVSSG 120
 DB 61 ADDFKRFAFSLSTASTAYLQINLNKNEIDTATFCARKDL-RYFDYWGQGTIVTVSSG 119

QY 121 GSGGGSGGGSGGGSETTLTQSPFLSAFVGDRTITTCRAPSGIRNLIAMVQKRGKAPK- 179
 DB 120 GSGGGSGGGSGGGSDIELTQSPSLASLGKVTITCKASQDINKYIAMVQKRGKAPK- 179

QY 180 ---LLIYAASLTQSGVPSRFSFGSGGTDFLTITSLQPDPAITYCCQYNSYPLSPFGGCT 236
 DB 180 ARTLHIY----IOPGISRFSFGSGGRDYSFSLNLEPDIAITYCLHIDNLH-TTCGGT 234

QY 237 KVEIKR 242
 DB 235 KLEIKR 240

RESULT 7
 ID 07TOM2 PRELIMINARY; PRT; 243 AA.

AC 07TOM2;
 DT 01-OCT-2003 (T-EMBLrel. 25, Created)
 DT 01-OCT-2003 (T-EMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 DE scFv 6H8 protein (Fragment).
 GN Name=scFv 6H8;

Query Match	57.9%;	Score 733;	DB 2;	Length 243;
Best Local Similarity	58.9%;	Pred. No. 4.2e-50;		
Matches 142;	Conservative 39;	Mismatches 56;	Indels 4;	Gaps 2;

RESULT 8
Q65ZL2
ID Q65ZL2 PRELIMINARY; PRT; 487 AA.

DT 25-OCT-2004 (TREMblrel. 28, Created)
 DT 25-OCT-2004 (TREMblrel. 28, Last sequence update)
 DT 25-OCT-2004 (TREMblrel. 28, Last annotation update)
 DE FV/M4.
 GN Name=M4-IFN-<tau>;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 OX NCBI_TaxID=10095;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96272580; PubMed=8668499;
 RA Qi Y., Xiang J.;
 RT "A genetically engineered single-gene-encoded anti-TAG72 chimeric
 RT antibody secreted from myeloma cells.";
 RL Hum. Antibodies Hybridomas 6:161-166(1995).
 DR EMBL, S82493; AAB37424.2; -.
 DR InterPro: IPR003599; Ig.
 DR InterPro: IPR007110; Ig-1like.
 DR InterPro: IPR003587; Ig_c1.
 DR InterPro: IPR003598; Ig_c2.
 DR InterPro: IPR003006; Ig_MHC.
 DR InterPro: IPR003596; Ig_V.

Query Match	57.4%;	Score 727;	DB 2;	Length 487;
Best Local Similarity	56.4%;	Pred. No. 2.7e-49;		
Matches 136;	Conservative 43;	Mismatches 56;	Indels 6;	Gaps 2

RESULT 9
Q925S1
ID Q925S1 PRELIMINARY; PRT; 218 AA

DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE MRPS (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10099;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RX PubMed=11819679;
RA Su C. D., Zeng G., Yan X., Wang F., Tian F., Ren D., Zhao T., Li X.,
RA Su C. J;
RT "Mechanism of exogenous nucleic acids and their precursors improving
RT the repair of intestinal epithelium after irradiation in mice.";
RL World J. Gastroenterol. 6:709-717(2000).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/c;
RA Cui D., Zeng G., Yan X., Li X., Su C. J;
RT "Cloning of mouse genes related to repairing of intestinal epithelium
RT of the irradiated mice by treatment with the intestinal RNA of mice of
RT the same strain.";
RL Int. J. Radiat. Biol. Relat. Stud. Phys. Chem. Med. 19:71-80(2001).
DR EMBL; AF240168; AAK43733.1; -.
DR HSSP; P01665; IONZ.
DR SMART; SMO0406; IGV; 1.
DR PROSITE; PSS0835; IG_LIKE; 1.
FT NON TER 218 218
SQ SEQUENCE 218 AA; 23013 MW; 52E74EA8F7982817 CRC64;

Query Match	47.2%;	Score 598.5;	DB 2;	Length 218;
Best Local Similarity	53.5%;	Pred. No. 1.6e-39;		

GN Name=DKFZp686C11235;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Human small intestine;
 RG The German Human cDNA Consortium;
 RA Bloeker H., Becher M., Mewes H.W., Weil B., Amlid C., Osanger A.,
 RA Fobg G., Han M., Wiemann S.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BK640853; CAB45920.1; -
 DR HSSP; P01861; IADQ.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR007110; IG_Like.
 DR InterPro; IPR003597; IG_C1.
 DR InterPro; IPR003006; IG_MHC.
 DR InterPro; IPR003596; IG_V.
 DR Pfam; PF07654; C1-set; 3.
 DR SMART; SM00409; IG; 2.
 DR SMART; SM00407; IG; 1; 3.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_2.
 DR Hypothetical protein.
 SQ SEQUENCE 473 AA; 52121 MW; 9476EAE4C0BFC447 CRC64;

Query Match 39.1%; Score 498; DB 2; Length 473;
 Best Local Similarity 46.8%; Pred. No. 3.4e-31;
 Matches 118; Conservative 30; Mismatches 58; Indels 46; Gaps 9;
 QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMGVROAPKGLFVWVSISGSSRYIY 60
 DB 20 ELQVLESGGGLVQPGGSLRLSCAASGFTSSYFEMNVRQAPKGLFVWVSISGSSRYIY 79
 QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADDAVYVCAKMDASG--SYFNFWGGGLTV 115
 DB 80 ADSVGRFTISRDNKNTLYLQNSLRADDAVYVCAKMDASG--SYFNFWGGGLTV 139
 QY 116 TVSSGGGGGGGGGGGGSTTTLTQSPPSLPSAVGRIITTCASRG--IRNVLAVYQOK 173
 DB 140 TVSSASG-----TKGSPVPLAPSSKSTSGTAALGCLVKDFL----- 177
 QY 174 PKAPKLLIYAASLTQSGV---PSRPSGSG---SGTDFLTTLISLPEDPATYVCOQVNS 227
 DB 178 ---EPTVSMNSALTSVGHITPAVYVLOSGLYLSVSVYVPSLSLGTQ---TTC-NVNH 230
 QY 228 YPLSPGGGKTVE 239
 DB 231 KP-----SNTKVD 238

RESULT 13
 Q8WUK1 PRELIMINARY; PRT; 613 AA.
 AC Q8WUK1;
 DT 01-MAR-2002 (TrEMBLrel. 20, Created)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE IGHM protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahney J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butlerfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalls D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Marra M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002);
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Primary B-Cells;
 RA Strausberg R.;
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC020240; AAH20240.1; -
 DR PIR; F36005; F36005.
 DR PIR; G36005; G36005.
 DR PIR; PH1642; PH1642.
 DR PIR; PH1643; PH1643.
 DR PIR; PH1645; PH1645.
 DR PIR; PH1646; PH1646.
 DR PIR; P10098; P10098.
 DR PIR; P10120; P10120.
 DR PIR; S15590; S15590.
 DR PIR; S31116; S31116.
 DR PIR; S31119; S31119.
 DR PIR; S70442; S70442.
 DR HSSP; P01861; IADQ.
 DR Pfam; PF07654; C1-set; 4.
 DR SMART; SM00406; IG; 1.
 DR PROSITE; PS50835; IG_LIKE; 5.
 DR PROSITE; PS00290; IG_MHC; UNKNOWN_3.
 SQ SEQUENCE 613 AA; 67295 MW; 60C7F5950671E315 CRC64;

Query Match 39.1%; Score 495.5; DB 2; Length 613;
 Best Local Similarity 64.0%; Pred. No. 7.2e-31;
 Matches 110; Conservative 8; Mismatches 27; Indels 27; Gaps 4;
 QY 1 QVQLVESGGGLVQPGGSLRLSCAASGFTSSYAMGVROAPKGLFVWVSISGSSRYIY 60
 DB 20 ELQVLESGGGLVQPGGSLRLSCAASGFTSSYGMNVRQAPKGLFVWVSISGSSRYIY 79
 QY 61 ADSVKGRFTISRDNKNTLYLQNSLRADDAVYVCAKMDASG--SYFNFWGGGLTV 119
 DB 80 ADSVGRFTISRDNKNTLYLQNSLRADDAVYVCAKMDASG--SYFNFWGGGLTV 139
 QY 120 GGGGGGGGGGGGGSTTTLTQSPPSLPSAVGRIITTCASRG--IRNVLAVYQOK 156
 DB 140 -----GSASAPTLPLVSCENSPDTSVAVGCLADFLPDSITFS 180

RESULT 14
 Q96K68 PRELIMINARY; PRT; 494 AA.
 AC Q96K68;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein FLJ14473.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Mammary gland;

I HIS PAGE BLANK (USPTO)